Figure 1. Nucleotide sequence including the sequence encoding the aortic carboxypeptidase-like protein of the invention.

GCGGGGGGCAGGAAGGGGCGGGGGGCTCGGCGCACTCGGCAGGAAGAGACCGACCCG
CCACCCGCCGTAGCCCGCGCGCCCCTGGCACTCAATCCCCGCCATGTGGGGGCTCCTGC
TCGCCCTGGCCGCCTTCGCGCCGGCCGTCGGCCCGGCTCTGGGGGCGCCCAGGAACTCG
GTGCTGGGCCTCGCGCAGCCCGGGACCACCAAGGTCCCAGGCTCGACCCCGGCCCTGCA
TAGCAGCCCGGCACAGCCGCCGGCGGAGACAGCTAACGGGACCTCAGAACAGCATGTC
CGGATTCGAGTCATCAAGAAGAAAAAGGTCATTATGAAGAAGCGGAAGAAGCTAACTC
TAACTCGCCCCACCCCACTGGTGACTGCCGGGCCCCTTGTGACCCCCACTCCAGCAGGG
ACCCTCGACCCCGCTGAGAAACAAGAAACAGGCTGTCCTCCTTTGGGTCTGGAGTCCCT
GCGAGTTTCAGATAGCCGGCTTGAGGCATCCAGCAGCCAGTCCTTTGGTCTTGGACCAC
ACCGAGGACGGCTCAACATTCAGTCAGGCCTGGAGGACGGCGATCTATATGATGGAGC
CTGGTGTGCTGAGGAGCAGGACGCCGATCCATGGTTTCAGGTGGACGCTGGGCACCCCA
CCCGCTTCTCGGGTGTTATCACACAGGGCAGGAACTCTGTCTGGAGGTATGACTGGGTC
ACATCATACAAGGTCCAGTTCAGCAATGACAGTCGGACCTGGTGGGGAAGTAGGAACC
ACAGCAGTGGGATGGACGCAGTATTTCCTGCCAATTCAGACCCAGAAACTCCAGTGCTG
AACCTCCTGCCGGAGCCCCAGGTGGCCCGCTTCATTCGCCTGCTGCCCCAGACCTGGCT
CCAGGGAGGCGCGCCTTGCCTCCGGGCAGAGATCCTGGCCTGCCCAGTCTCAGACCCCA
ATGACCTATTCCTTGAGGCCCCTGCGTCGGGATCCTCTGACCCTCTAGACTTTCAGCATC
ACAATTACAAGGCCATGAGGAAGCTGATGAAGCAGGTACAAGAGCAATGCCCCAACAT
CACCCGCATCTACAGCATTGGGAAGAGCTACCAGGGCCTGAAGCTGTATGTGATGGAA
ATGTCGGACAAGCCTGGGGAGCATGAGCTGGGGGAGCCTGAGGTGCGCTACGTGGCTG
GCATGCATGGGAACGAGGCCCTGGGGCGGGAGTTGCTTCTGCTCCTGATGCAGTTCCTG
TGCCATGAGTTCCTGCGAGGGAACCCACGGGTGACCCGGCTGCTCTCTGAGATGCGCAT
TCACCTGCTGCCCTCCATGAACCCTGATGGCTATGAGATCGCCTACCACCGGGGTTCAG
AGCTGGTGGGCTGGGCCGAGGGCCGCTGGAACAACCAGAGCATCGATCTTAACCATAA
TTTTGCTGACCTCAACACACCACTGTGGGAAGCACAGGACGATGGGAAGGTGCCCCACA
TCGTCCCCAACCATCACCTGCCATTGCCCACTTACTACACCCTGCCCAATGCCACCGTGG
CTCCTGAAACGCGGGCAGTAATCAAGTGGATGAAGCGGATCCCCTTTGTGCTAAGTGCC
AACCTCCACGGGGGTGAGCTCGTGGTGTCCTACCCATTCGACATGACTCGCACCCCGTG
GGCTGCCCGCGAGCTCACGCCCACACCAGATGATGCTGTGTTTCGCTGGCTCAGCACTG
TCTATGCTGGCAGTAATCTGGCCATGCAGGACACCAGCCGCCGACCCTGCCACAGCCAG
GACTTCTCCGTGCACGGCAACATCATCAACGGGGCTGACTGGCACACGGTCCCCGGGAG
CATGAATGACTTCAGCTACCTACACACCAACTGCTTTGAGGTCACTGTGGAGCTGTCCT
GTGACAAGTTCCCTCACGAGAATGAATTGCCCCAGGAGTGGGAGAACAACAAAGACGC
CCTCCTCACCTACCTGGAGCAGGTGCGCATGGGCATTGCAGGAGTGGTGAGGGACAAG
GACACGGAGCTTGGGATTGCTGACGCTGTCATTGCCGTGGATGGGATTAACCATGACGT
GACCACGGCGTGGGGCGGGGATTATTGGCGTCTGCTGACCCCAGGGGACTACATGGTG
ACTGCCAGTGCCGAGGGCTACCATTCAGTGACACGGAACTGTCGGGTCACCTTTGAAGA
GGGCCCCTTCCCCTGCAATTTCGTGCTCACCAAGACTCCCAAACAGAGGCTGCGCGAGC
TGCTGGCAGCTGGGGCCAAGGTGCCCCCGGACCTTCGCAGGCGCCTGGAGCGGCTAAG
GGGACAGAAGGATTGATACCTGCGGTTTAAGAGCCCTAGGGCAGGCTGGACCTGTCAA
GACGGGAAGGGGAAGAGTAGAGAGGGAGGGACAAA

Figure 2. Protein sequence encoded by the coding sequence shown in Figure 1.

MWGLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETA
NGTSEQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQET
GCPPL**GLESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEE**
QDADPWFQVDAGHPTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGS
RNHSSGMDAVFPANSDPETPVLNLLPEPQVARFIRLLPQTWLQGGAPCLRAEIL
ACPVSDPNDLFLEAPASGSSDPLDF*QHHNYKAMRKLMKQVQEQCPNITRIYSIGKSYQ*
GLKLYVMEMSDKPGEHELGEPEVRYVAGMHGNEALGRELLLLLMQFLCHEFLRGNPRV
*TRLLSEMRIHLLPSMNPDGYE*IAYHRGSELVGWAEGRWNNQSIDLNHNFADLNTPLW
EAQDDGKVPHIVPNHHLPLPTYYTLPNATVAPETRAVIKWMKRIPFVLSANLHGGE
LVVSYPFDMTRTPWAARELTPTPDDAVFRWLSTVYAGSNLAMQDTSRRPCHSQDF
SVHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHENELPQEWENNKD
ALLTYLEQVRMGIAGVVRDKDTELGIADAVIAVDGINHDVTTAWGGDYWRLLTPG
DYMVTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPPDLR
RRLERLRGQKD

Figure 3. ClustalW alignment of a protein of the invention.

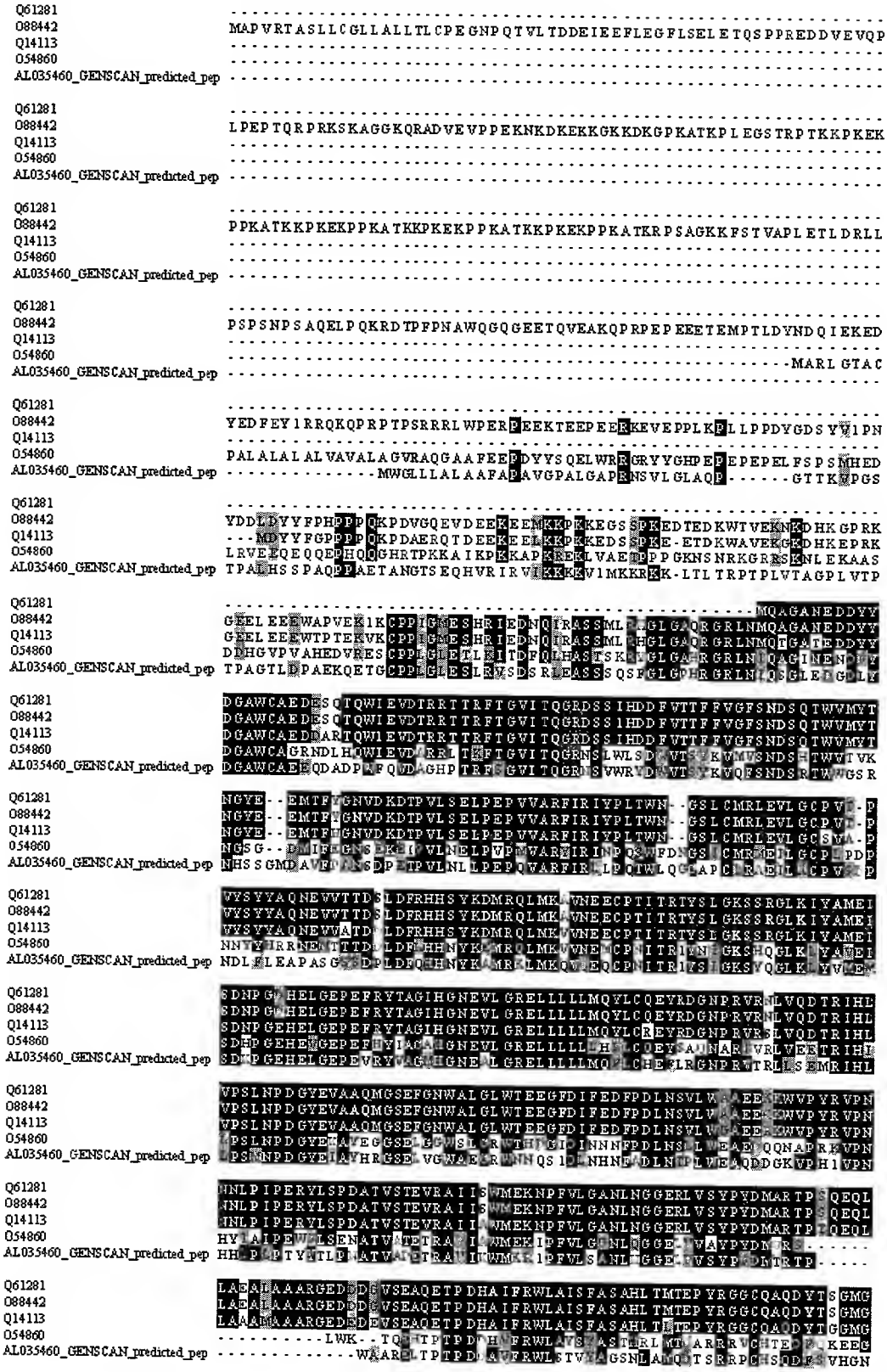


Figure 4: ClustalW Alignment of protein sequences (Mouse CPX1 vs AL035460_A).

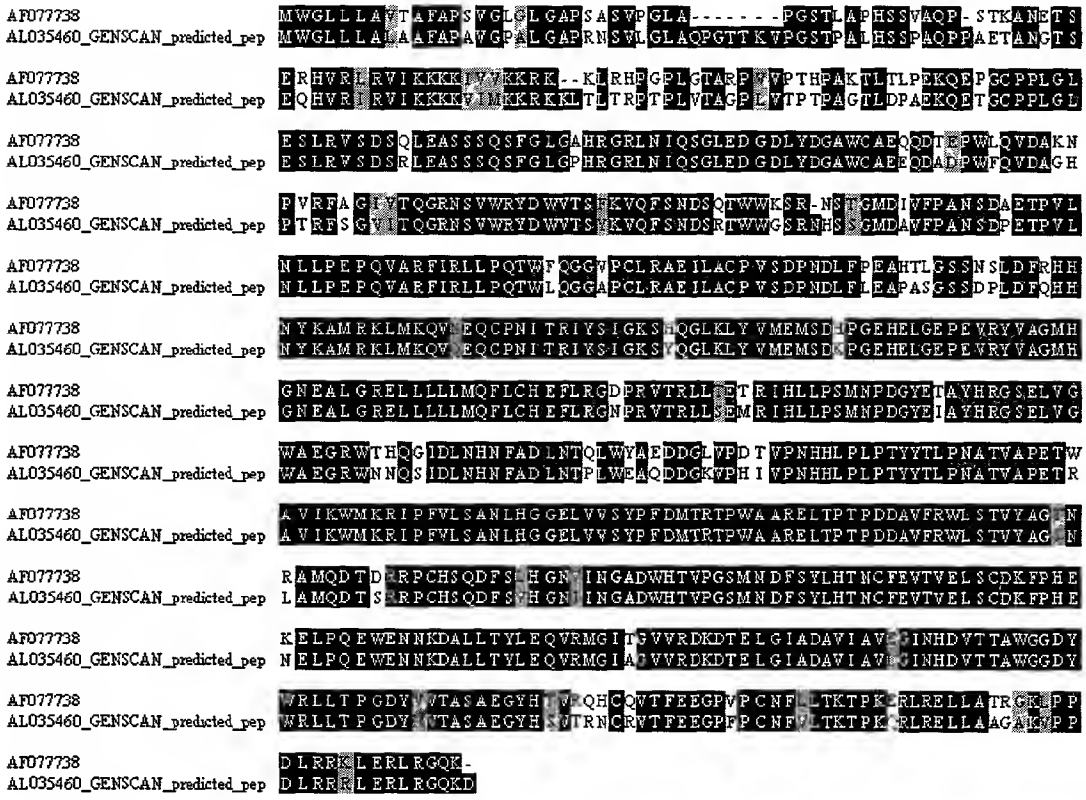
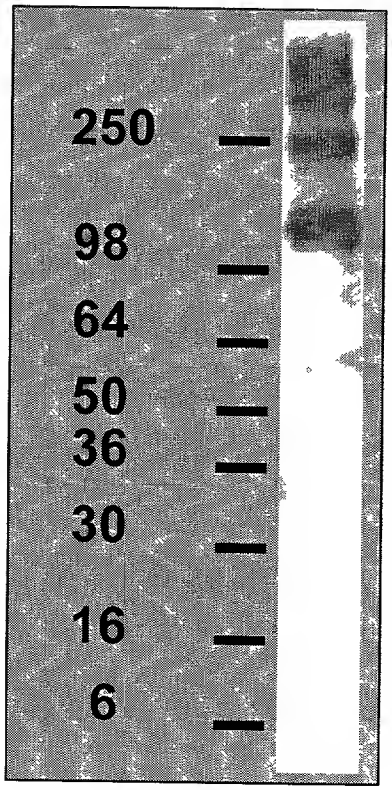


Figure 5. Western blot SDS-PAGE of hAL035460A protein secreted by 293 cells.



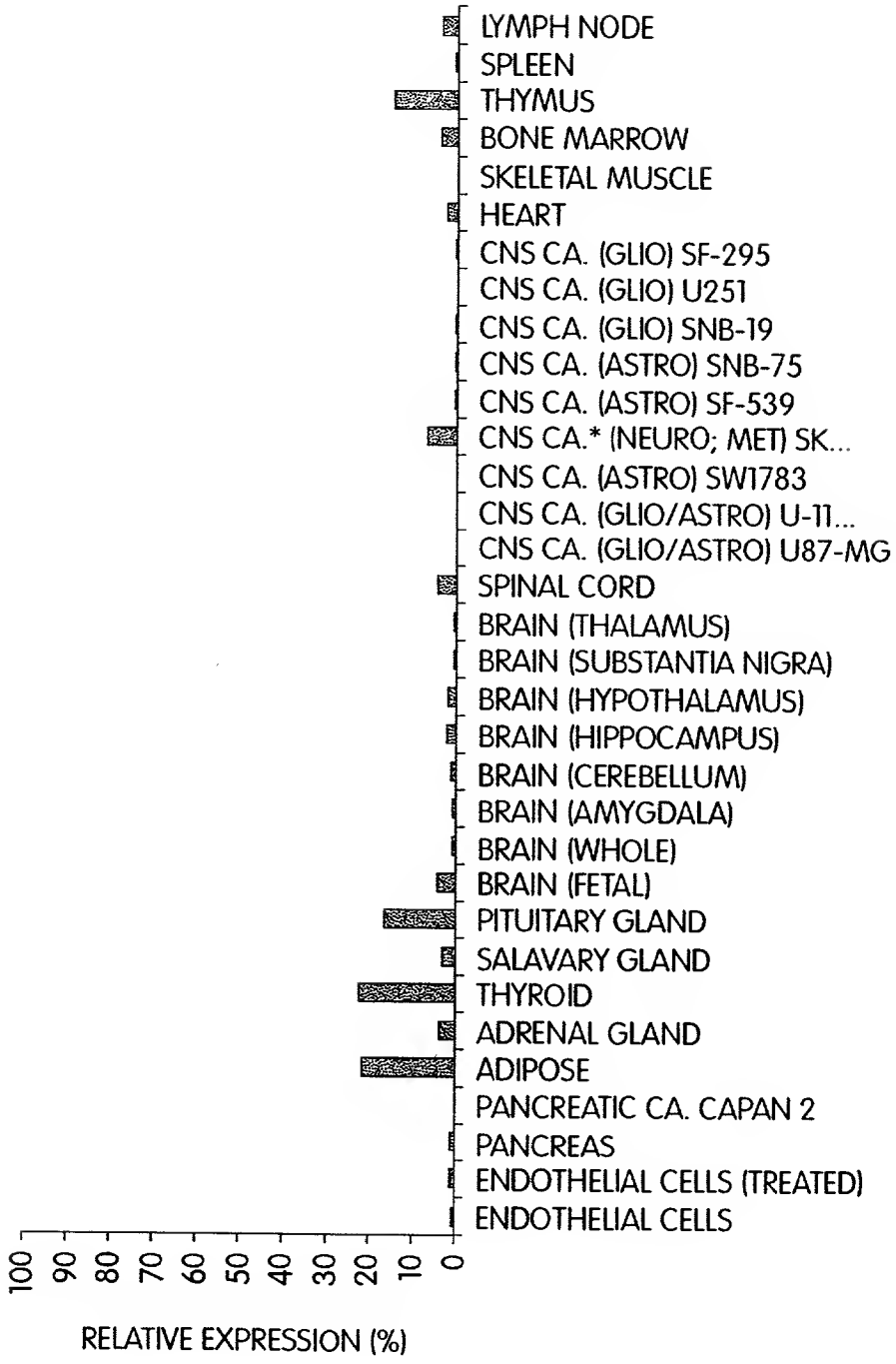

LYMPH NODE
SPLEEN
THYMUS
BONE MARROW
SKELETAL MUSCLE
HEART
CNS CA. (GLIO) SF-295
CNS CA. (GLIO) U251
CNS CA. (GLIO) SNB-19
CNS CA. (ASTRO) SNB-75
CNS CA. (ASTRO) SF-539
CNS CA.* (NEURO; MET) SK...
CNS CA. (ASTRO) SW1783
CNS CA. (GLIO/ASTRO) U-11...
CNS CA. (GLIO/ASTRO) U87-MG
SPINAL CORD
BRAIN (THALAMUS)
BRAIN (SUBSTANTIA NIGRA)
BRAIN (HYPOTHALAMUS)
BRAIN (HIPPOCAMPUS)
BRAIN (CEREBELLUM)
BRAIN (AMYGDALA)
BRAIN (WHOLE)
BRAIN (FETAL)
PITUITARY GLAND
SALAVARY GLAND
THYROID
ADRENAL GLAND
ADIPOSE
PANCREATIC CA. CAPAN 2
PANCREAS
ENDOTHELIAL CELLS (TREATED)
ENDOTHELIAL CELLS
100 90 80 70 60 50 40 30 20 10 0
RELATIVE EXPRESSION (%)
TISSUE SOURCE

Fig. 6A

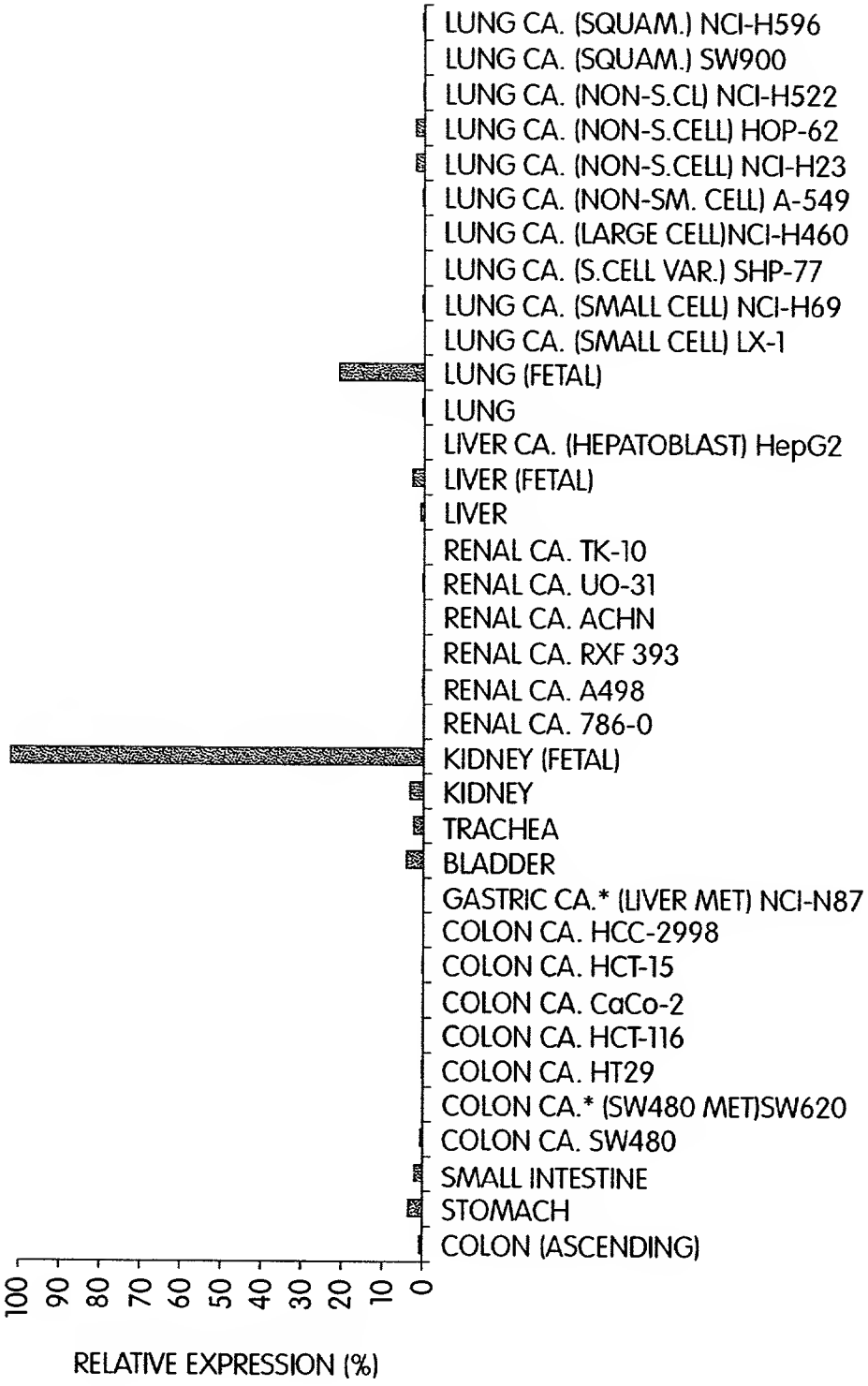

LUNG CA. (SQUAM.) NCI-H596
LUNG CA. (SQUAM.) SW900
LUNG CA. (NON-S.CL) NCI-H522
LUNG CA. (NON-S.CELL) HOP-62
LUNG CA. (NON-S.CELL) NCI-H23
LUNG CA. (NON-SM. CELL) A-549
LUNG CA. (LARGE CELL)NCI-H460
LUNG CA. (S.CELL VAR.) SHP-77
LUNG CA. (SMALL CELL) NCI-H69
LUNG CA. (SMALL CELL) LX-1
LUNG (FETAL)
LUNG
LIVER CA. (HEPATOBLAST) HepG2
LIVER (FETAL)
LIVER
RENAL CA. TK-10
RENAL CA. UO-31
RENAL CA. ACHN
RENAL CA. RXF 393
RENAL CA. A498
RENAL CA. 786-0
KIDNEY (FETAL)
KIDNEY
TRACHEA
BLADDER
GASTRIC CA.* (LIVER MET) NCI-N87
COLON CA. HCC-2998
COLON CA. HCT-15
COLON CA. CaCo-2
COLON CA. HCT-116
COLON CA. HT29
COLON CA.* (SW480 MET)SW620
COLON CA. SW480
SMALL INTESTINE
STOMACH
COLON (ASCENDING)
100
90
80
70
60
50
40
30
20
10
0
RELATIVE EXPRESSION (%)
TISSUE SOURCE

Fig. 6B

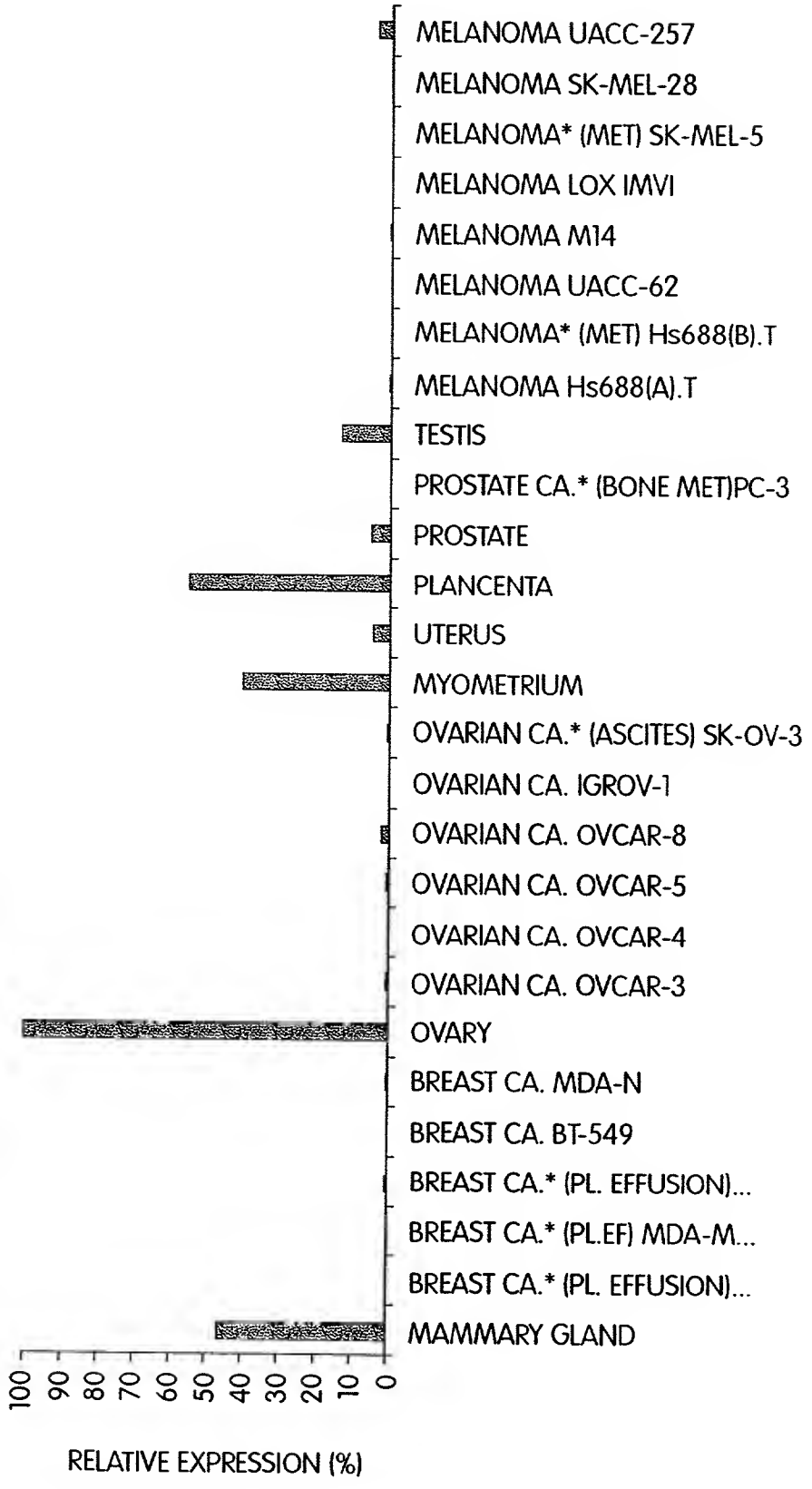

MELANOMA UACC-257
MELANOMA SK-MEL-28
MELANOMA* (MET) SK-MEL-5
MELANOMA LOX IMVI
MELANOMA M14
MELANOMA UACC-62
MELANOMA* (MET) Hs688(B).T
MELANOMA Hs688(A).T
TESTIS
PROSTATE CA.* (BONE MET)PC-3
PROSTATE
PLANCENTA
UTERUS
MYOMETRIUM
OVARIAN CA.* (ASCITES) SK-OV-3
OVARIAN CA. IGROV-1
OVARIAN CA. OVCAR-8
OVARIAN CA. OVCAR-5
OVARIAN CA. OVCAR-4
OVARIAN CA. OVCAR-3
OVARY
BREAST CA. MDA-N
BREAST CA. BT-549
BREAST CA.* (PL. EFFUSION)...
BREAST CA.* (PL.EF) MDA-M...
BREAST CA.* (PL. EFFUSION)...
MAMMARY GLAND
100 90 80 70 60 50 40 30 20 10 0
RELATIVE EXPRESSION (%)
TISSUE SOURCE

Fig. 6C

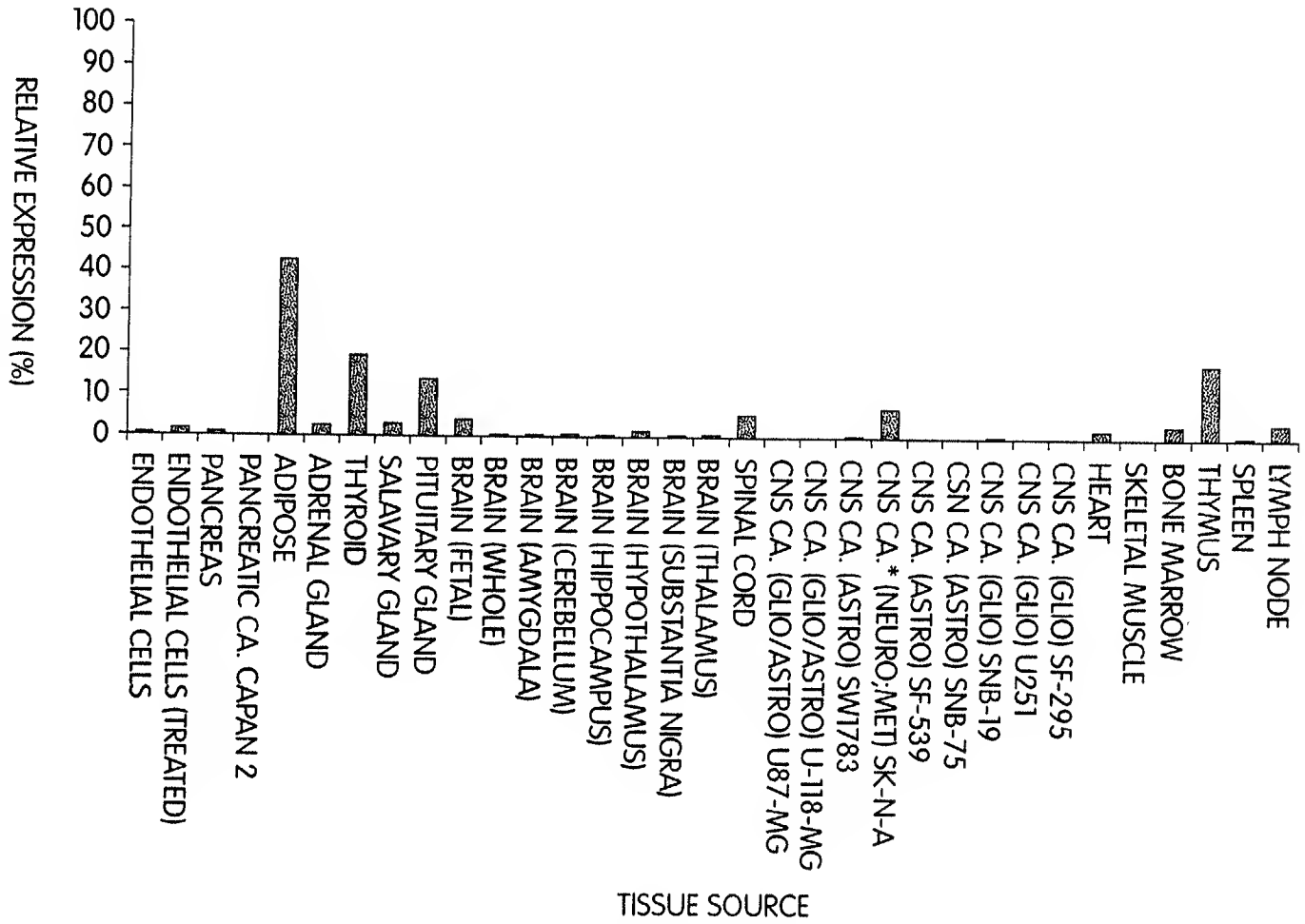

RELATIVE EXPRESSION (%)
100
90
80
70
60
50
40
30
20
10
0
ENDOTHELIAL CELLS
ENDOTHELIAL CELLS (TREATED)
PANCREAS
PANCREATIC CA. CAPAN 2
ADIPOSE
ADRENAL GLAND
SALAVARY GLAND
THYROID
PITUITARY GLAND
BRAIN (FETAL)
BRAIN (WHOLE)
BRAIN (AMYGDALA)
BRAIN (CEREBELLUM)
BRAIN (HIPPOCAMPUS)
BRAIN (HYPOTHALAMUS)
BRAIN (SUBSTANTIA NIGRA)
BRAIN (THALAMUS)
SPINAL CORD
CNS CA. (GLIO/ASTRO) U87-MG
CNS CA. (GLIO/ASTRO) U-118-MG
CNS CA. (ASTRO) SW1783
CNS CA.* (NEURO;MET) SK-N-A
CNS CA. (ASTRO) SF-539
CSN CA. (ASTRO) SNB-75
CNS CA. (GLIO) SNB-19
CNS CA. (GLIO) U251
CNS CA. (GLIO) SF-295
HEART
SKELETAL MUSCLE
BONE MARROW
THYMUS
SPLEEN
LYMPH NODE
TISSUE SOURCE

Fig. 7A

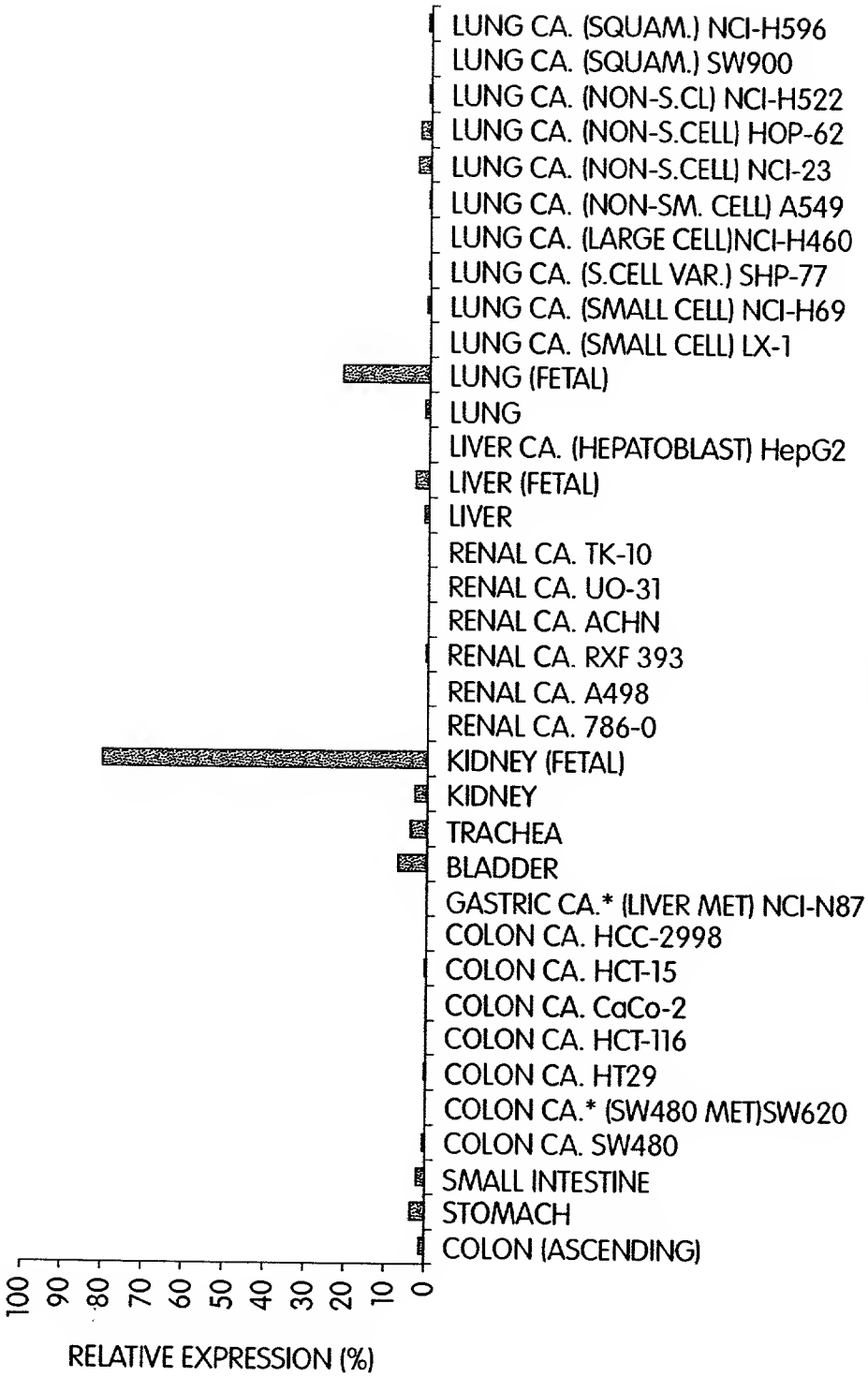

LUNG CA. (SQUAM.) NCI-H596
LUNG CA. (SQUAM.) SW900
LUNG CA. (NON-S.CL) NCI-H522
LUNG CA. (NON-S.CELL) HOP-62
LUNG CA. (NON-S.CELL) NCI-23
LUNG CA. (NON-SM. CELL) A549
LUNG CA. (LARGE CELL)NCI-H460
LUNG CA. (S.CELL VAR.) SHP-77
LUNG CA. (SMALL CELL) NCI-H69
LUNG CA. (SMALL CELL) LX-1
LUNG (FETAL)
LUNG
LIVER CA. (HEPATOBLAST) HepG2
LIVER (FETAL)
LIVER
RENAL CA. TK-10
RENAL CA. UO-31
RENAL CA. ACHN
RENAL CA. RXF 393
RENAL CA. A498
RENAL CA. 786-0
KIDNEY (FETAL)
KIDNEY
TRACHEA
BLADDER
GASTRIC CA.* (LIVER MET) NCI-N87
COLON CA. HCC-2998
COLON CA. HCT-15
COLON CA. CaCo-2
COLON CA. HCT-116
COLON CA. HT29
COLON CA.* (SW480 MET)SW620
COLON CA. SW480
SMALL INTESTINE
STOMACH
COLON (ASCENDING)
TISSUE SOURCE
100
90
80
70
60
50
40
30
20
10
0
RELATIVE EXPRESSION (%)

Fig. 7B

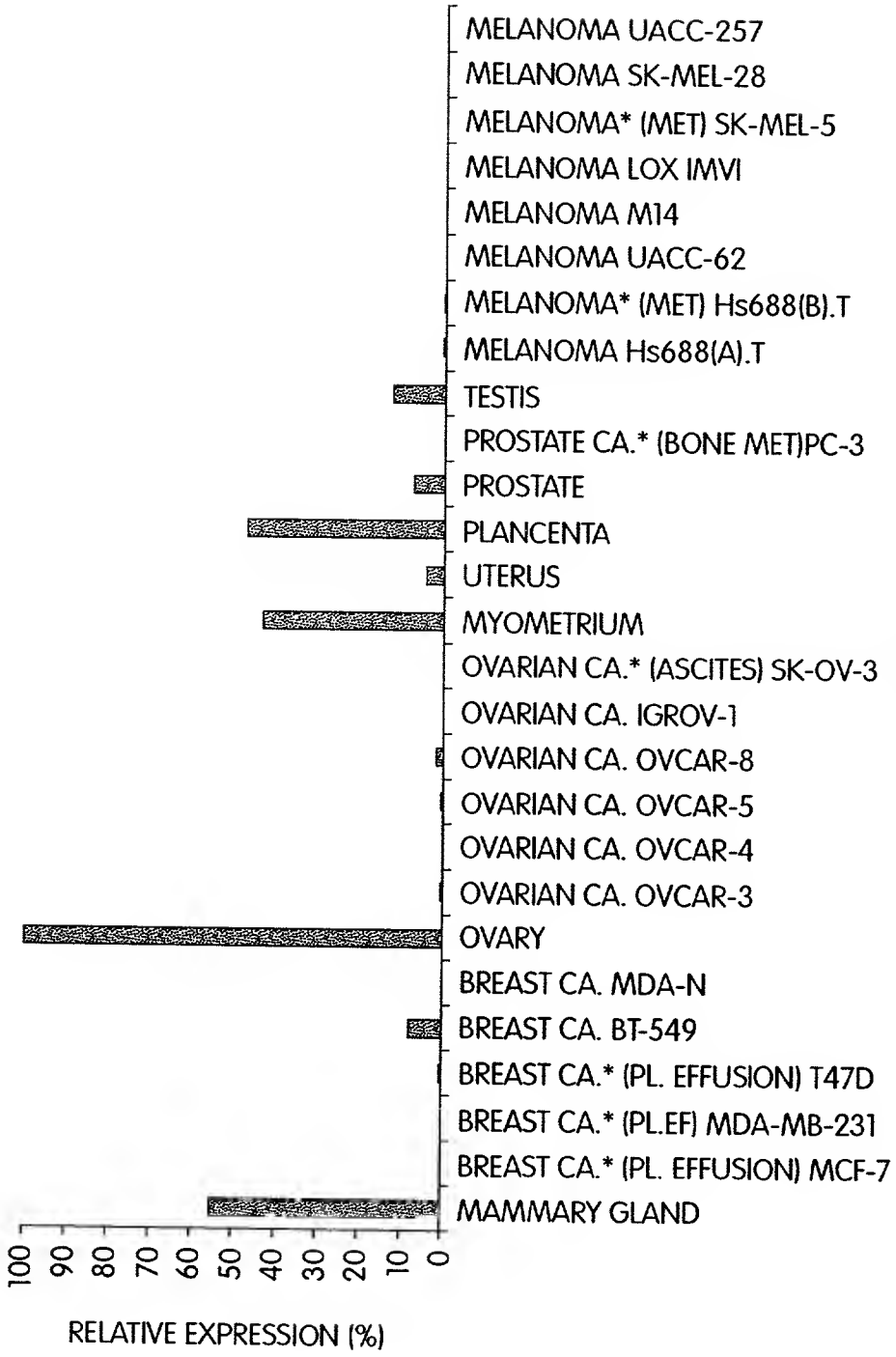

MELANOMA UACC-257
MELANOMA SK-MEL-28
MELANOMA* (MET) SK-MEL-5
MELANOMA LOX IMVI
MELANOMA M14
MELANOMA UACC-62
MELANOMA* (MET) Hs688(B).T
MELANOMA Hs688(A).T
TESTIS
PROSTATE CA.* (BONE MET)PC-3
PROSTATE
PLANCENTA
UTERUS
MYOMETRIUM
OVARIAN CA.* (ASCITES) SK-OV-3
OVARIAN CA. IGROV-1
OVARIAN CA. OVCAR-8
OVARIAN CA. OVCAR-5
OVARIAN CA. OVCAR-4
OVARIAN CA. OVCAR-3
OVARY
BREAST CA. MDA-N
BREAST CA. BT-549
BREAST CA.* (PL. EFFUSION) T47D
BREAST CA.* (PL.EF) MDA-MB-231
BREAST CA.* (PL. EFFUSION) MCF-7
MAMMARY GLAND
100 90 80 70 60 50 40 30 20 10 0
RELATIVE EXPRESSION (%)
TISSUE SOURCE

Fig. 7C

Figure 8

>CG54007-01 20190 nt

ATGTGGGGGCTCCTGCTCGCCCTGGCCGCCTTCGCGCCGGCCGTCGGCCCGGCTCTGGGG
GCGCCCAGGAACTCGGTGCTGGGCCTCGCGCAGCCCGGGACCACCAAGGTCCCAGGCTCG
ACCCCGGCCCTGCATAGCAGCCCGGCACAGCCGCCGGCGGAGACAGCTAACGGGACCTCA
GAACAGCATGTCCGGATTCGAGTCATCAAGAAGAAAAAGGTCATTATGAAGAAGCGGAAG
AAGCTAACTCTAACTCGCCCCACCCCACTGGTGACTGCCGGGCCCCTTGTGACCCCCACT
CCAGCAGGGACCCTCGACCCCGCTGAGAAACAAGAAACAGGCTGTCCTCCTTTGGGTCTG
GAGTCCCTGCGAGTTTCAGATAGCCGGCTTGAGGCATCCAGCAGCCAGTCCTTTGGTCTT
GGACCACACCGAGGACGGCTCAACATTCAGTCAGGCCTGGAGGACGGCGATCTATATGAT
GGAGCCTGGTGTGCTGAGGAGCAGGACGCCGATCCATGGTTTCAGGTGGACGCTGGGCAC
CCCACCCGCTTCTCGGGTGTTATCACACAGGGCAGGAACTCTGTCTGGAGGTATGACTGG
GTCACATCATACAAGGTCCAGTTCAGCAATGACAGTCGGACCTGGTGGGGAAGTAGGAAC
CACAGCAGTGGGATGGACGCAGTATTTCCTGCCAATTCAGACCCAGAAACTCCAGTGCTG
AACCTCCTGCCGGAGCCCCAGGTGGCCCGCTTCATTCGCCTGCTGCCCCAGACCTGGCTC
CAGGGAGGCGCGCCTTGCCTCCGGGCAGAGATCCTGGCCTGCCCAGTCTCAGACCCCAAT
GACCTATTCCTTGAGGCCCCTGCGTCGGGATCCTCTGACCCTCTAGACTTTCAGCATCAC
AATTACAAGGCCATGAGGAAGCTGATGAAGCAGGTACAAGAGCAATGCCCCAACATCACC
CGCATCTACAGCATTGGGAAGAGCTACCAGGGCCTGAAGCTGTATGTGATGGAAATGTCG
GACAAGCCTGGGGAGCATGAGCTGGGGGAGCCTGAGGTGCGCTACGTGGCTGGCATGCAT
GGGAACGAGGCCCTGGGGCGGGAGTTGCTTCTGCTCCTGATGCAGTTCCTGTGCCATGAG
TTCCTGCGAGGGAACCCACGGGTGACCCGGCTGCTCTCTGAGATGCGCATTCACCTGCTG
CCCTCCATGAACCCTGATGGCTATGAGATCGCCTACCACCGGGGTTCAGAGCTGGTGGGC
TGGGCCGAGGGCCGCTGGAACAACCAGAGCATCGATCTTAACCATAATTTTGCTGACCTC
AACACACCACTGTGGGAAGCACAGGACGATGGGAAGGTGCCCCACATCGTCCCCAACCAT
CACCTGCCATTGCCCACTTACTACACCCTGCCCAATGCCACCGTGGCTCCTGAAACGCGG
GCAGTAATCAAGTGGATGAAGCGGATCCCCTTTGTGCTAAGTGCCAACCTCCACGGGGGT
GAGCTCGTGGTGTCCTACCCATTCGACATGACTCGCACCCCGTGGGCTGCCCGCGAGCTC
ACGCCCACACCAGATGATGCTGTGTTTCGCTGGCTCAGCACTGTCTATGCTGGCAGTAAT
CTGGCCATGCAGGACACCAGCCGCCGACCCTGCCACAGCCAGGACTTCTCCGTGCACGGC
AACATCATCAACGGGGCTGACTGGCACACGGTCCCCGGGAGCATGAATGACTTCAGCTAC
CTACACACCAACTGCTTTGAGGTCACTGTGGAGCTGTCCTGTGACAAGTTCCCTCACGAG
AATGAATTGCCCCAGGAGTGGGAGAACAACAAAGACGCCCTCCTCACCTACCTGGAGCAG
GTGCGCATGGGCATTGCAGGAGTGGTGAGGGACAAGGACACGGAGCTTGGGATTGCTGAC
GCTGTCATTGCCGTGGATGGGATTAACCATGACGTGACCACGGCGTGGGGCGGGGATTAT
TGGCGTCTGCTGACCCCAGGGGACTACATGGTGACTGCCAGTGCCGAGGGCTACCATTCA
GTGACACGGAACTGTCGGGTCACCTTTGAAGAGGGCCCCTTCCCCTGCAATTTCGTGCTC
ACCAAGACTCCCAAACAGAGGCTGCGCGAGCTGCTGGCAGCTGGGGCCAAGGTGCCCCCG
GACCTTCGCAGGCGCCTGGAGCGGCTAAGGGGACAGAAGGATTGANNANTNCANNTTNAN
NNTNGNNANNTCTCACTTATAAATGGAAGCTGGCGGGACACGGTGGCTCACTCCTGTAAT
CCCAACACTTTGGGAGGCTGAGGCGGGTGGATCACGAGGTCAGGAGATCGAGACCATCCT
GACTAACACGGTGAAACCCGTCTCTACTAAAAACACAAAAAATTAGCTGGGCGTGGTGGC
GGCACCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATGGCATGAACCCAGGAG
TCGGAGCTTGCAGTGAGCCGAGTTCACGCCACTGCATTCCAGCCTGGGCAACAGAGCGAG
ACTCTGTCTCAAAAAAAATAAATTAAATAAAAATAAATAAATGGAAACTAAGCTGTGGGT
ATGCAAAGGCATACAGAATGGTATAATGGACATTGGAGACTCAGAAGGAGGAGGGTAAGC
GGGGGGTGACAGATAAAAAAAACTGCATGTTGCATACAATGTACACTACTCGGGTGATGG
GCGCTCTAAGATTTCAAACTTCACCACTATACAGTTCTCCCCTGTAACCAAAAACCGCTG
GTACCCCTAAAGCAATTGAAATAAAAATAGAAACTATGTTGTAGCCTGGATGACATAGCG

AAAACTTGTCTCTTAAAAAAAAAAAAATGTGGCCGGGTGCAGTGGCTCACACCTGTAATC
CCAGCACTTTGGGAGGCCCAAGGCGGGCAGATCACAAGGTCAGGAGATTGAGACCGTCCT
GGCTAACAAGGTGAAACTCCATCTCTACTAAAAATACAAAAAATTAGCCGGGTGTGGTGG
CACACGCCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGA
GGCGGAGGTTGCAGTGAGCCGAGATCGCACCACAGCACTCCAGCCTGGTGACAGAGTGAG
ATTTAGTCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGTAGAAATTAGCTGAGCGTG
GTGACACGTCCCAGATACTTGGGAGGCTGAGGTGGGAGGATCGCTTGAACCCAGGAGTTC
CAGACTGCAGTGAGCTGTGATTACACTATTGCACTCCAGCCTAGGCTGTGGGAAAGAGAG
TTTCTGGGGTGCCAGCTGAGTTAGTCTTCCCTGTGTGAGACACCCATGGGAAGCCATGCG
CGGCCTCTGAGGAGAAAAGTCTCCTTATTGCCTTCATGTCTTTACGCCCGAGAGCAGAAC
CCCTCAGCGGCATTCCACAGGTTGCTCAGGCATATAACACTCCCTTGAAGCAGTGGAGTA
TAATCAAACATCTTGGCTCCTCCTGAAACCCACTCCCACCCGTTTCAGTCCCGATAAGTT
AAAGATTTGTTTTGTTTTGTTTTTGTTTGAGACGGAGTCTCGCTCTGTCGCCCAGGCTGG
AGTGCGGTGGCTCGATCTCGGCTCACTGCAAGCTCCGCCTCCCGGGTTCACGCCATTCTC
CCGCCTCAGCCTCCCGAGTAGCTGGGACGACAGGCGCCCGCCACCACGCCCGGCTAATTT
TTTGTATTTTTAGTAGAGACGGGGTTTCACCACGTTGGCCAGAGTGGTCTCGAACTCCTG
ACCTCAAGCGATCCACCCACCTCAGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCAC
CGCGCCCGGCCAGTTAAAGATCTTAAGTAGTTTGACACTCCTCTTTGCTCAAGGAAATTC
ACAGAAACCGCCACTGCTATACATCTTACAGAATGACTCTCCAGTTCTCCTTCACTGATT
AATCCTTTCCCTCATCCCTTCCTCCTCCTCCCATCTGCCCTAAGAACAAAGAGCTTGTAA
ACCAATAAATTGGGCGGAGCCTGAGAACTCTGGGCCGTGAGCAAGCCTCCGACGCTCCGG
TCCCCTGGACCCGCCTTTTAAACGCTTATTCTGTCTCTTTCTAACTCCTTTGTCTCCGCC
GGACTCGGGGTAACCGCTAGGCGTTATGGGGCTGTTTTCCCCAACATAGGCAACAGAGCA
GGACAGTGTCTCTAAAAAAACAAAACCAAAACTATATTTTGTACTATTCTGATAAAAATG
ACTTAGTTACAAACAAAGAACAAATCAACAGATAGTCATGCTGTGGAGATCAGGAATATT
CCTTCCCAGGGTAAATGAAAGACCAATTCCCTAACGTCATGTGGATATACGCTTGTGGCT
TAAGATAAAATTACCCGTGACAGCATCAAATACCAGGGATAAAACTCAGTCTTCAACACG
CATATGTATCTCCTGGGGTTGAATCCTCTGGAGGTCTTGTTAAAAATGCAGATTCTGGTC
AAGAGTTCGAGACCAGCCTGGCCAATATGGTGAAACCCTGTCTCTACTAAAAACACAAAA
ATTAGCTGGGTGTGGTGGTGGACGCCTGTAGTCCCAGCTACTCAGGAGACTGAGGCAGGA
GAATTGCTTGAACCCGGGAGGTGGCAGTTTAGTGAGCTGAGATCGGGCCACTGCACTCCA
GCCTGGGAGACAGAGTGAGACTCTGTCAAAAAAAAAAAAAAAAAAAAATGCATATTCTGA
TTCAATAGGTCTGGGGCAGAGGTGTTTTTTTTGTTTGTTTGTTTTTTGTTTTTTGGTTTT
TTTTTTGGTTTTTTTTTTTTGACAGAGTCTAGCTCTTTCACCTAGGCTGGAGTGCATGAC
ACCATCCCAGCTCACTGCAACCTCCGCTTCTTGGGTTCAAGCGATTCTCCTGCCTCAGCC
TCCTGAATAGCTGGGATTACAGGCGTGCACCACCACACCCAGCTAAGTTTTGTATTTGTA
GTAGAGATGGGGTTTCACCGTGTTGGCCAGGTAAGTTTTGTATTTGTATTTGGTCTTGAA
CTCCTGACCTCAGGTGATCCGCCCGCCTCGGCCTCCCAAAGTTCTGGGATTACAGGCGTG
AGCCACTGCACCCGGCCTGTTCTGCATTTCTAACAAGTTCCCAGGGGATGCTACTGCTGC
TGGTCTTCAACCACACTTTGTGGAGCAAGGCTCTCAAAGACCTTGATGTATGTAGGAGAG
AAAGCTGGGGTAGAGAGTGATGAGGGGAGAACGGGTGCGTGGGGAGATGCTCCCCTGTGC
ATCCTGGTCCCATGTGAGGCTCCAACAATGCTCACCTACATCACAGGGAGAGCACCTAGC
AGGAAATGAGTTCTGCTTTAGCATCCAGGCACAGGAGATTAGAGGCACAGGCAGGCAGTA
GATTCTACTTCATTATTTGTGCAGCTGGACACAGAGCTTCCTTTCTTTTCCTTGATACTG
TTTTATTCCATCTAAGTATGTAGGAGTAAGAGGGCTGTGTTACACTGTTTTCCCCACCTT
TAATGCATCTGATCAACCTAGGAGCCCCCTAAGACCCTATATTATCTCACTTTATCATCA
CAGCAAACCTGGGAGAAGGATATGGTTCCTGTTTTACAGATGAGGAAACTAAGTCTCAGG
GAGGTGAAACTACTGCCCAAGGATAGCCAAACAAAATACACGTCAGAAGTGGGATGTGAA
ACGAAGCCTGTATGTCACCAGAGTCACCTATCCTCTCCCCCTCCAACCACCTAACCACAC
CAGGGAGTTGGCAGGAGATTCCTAGCCCACCCCTTACATTAAAATCCCTTTTAGGCGGGT

GCCACTATCCAGTCCTTCTCAATTGCACCTAGTGAGACCACGAAAGATCTTCTACCTGGC
TCCTGGTAGATGAGATCTGGCTATACAGGTACTTGGGTGCAAACCTGCCCCTCTGCCCCT
GGAGCTATCACCTCCAGATCCTGCTACTTGTACCTTTGCAGCCCCAGGTAGCCAGTGGCA
AGGGCCAGGGGTGGCAGCAGGGCTGGGAGTGGAGAAGAGTGTGAGAAAGTGCTGCGGGGC
TCAGGAGACACAGCAGGGAACCAAGGGGTCCTAAGGGTTGCAATAGAGGACAGGGGCAGG
GAGTGCAGAGTGGTGGGAAGGGGGATGGGAGCTGGGTGCAGGAGACATAAGAGATGGAGC
ATCCCGGCCACACACGGTGGCTCACACCTGTTATCCCAGCACTTTGGGAGGCCGAGGTGG
GTGGATCACGAGGTCAGGAGATCGAGACCATCCTGGCTAACACGGTGAAACCCCGTCTCT
ACTAAAAACACAAAAAATTAGCCAGGCGAGGTGGTGTGCACCTGTAGTCCCAGCTTCTTG
GGAGGCTGAGGCAGGAGAATGGCGTGAACCCAGGAGGTGGAGCTTGCAGTCAGCTGAGAT
CCCGCCACTGCATTCCAGCCTGGGTGACAGAGTGAGACTCGTCTCAAAAAAAAAAAGAAT
AAAAGAAAAAAGAGGTGGAGCATCCTGCAGCCCTGGCCCCTAAAAGATTGGTGGGAGAGT
GCCAGCTGCTCCACCCTAGTCACTTTGGGAACTGGTCTTTCAGTTCACGGCCTGCCATGT
CCTCTCCTGCAAATCCTGGCACTGTTGAGGAGGTCCTTTCAGCCCTGGTTTGTCCACTCT
AACCTTGAATATATTATACACACACTTTATGAGAGCTGACGAGGGACCAGGTGCTGTTCT
AGGCTCTGAGGTGCAGCTGTGGACATTTGGGTACAAAGTTCTTCTGGCAGGGTACTTACC
TCCTGCTGGGGGTGGGGGAACCTGAACAGCCAACACATAAGTAAAGCAAGATCATCTCGG
TGTTGAGTGCCTTGAAGACAATAATTTAAACGGGTGGGAGGATAGAGTGTGTGAAGTGAA
AAAGTTTGCTTTAGTCAGGGTAGTCAGGGAAAGCCTTTGGGAGCAGGTGATATTGAAAGG
AAATCTGACTGAGAAGGCAAATTCCATGCACAAATTAAAAGGCCAGGAGGCTAGTTGGGC
TGTTGCGTGGGAGGAGCAGCTAGAATGCCGGAGTGACTGGGGGGATGGGAGCCAGGGGAT
AGGGAGGCAGATGGAATGGGAAAGGCGTGGGCAGGAAGAACTTGGTCATGAAGACCTTGC
AGGTGAACCCACTGGGGCCTTAAGCCTGGAGGAACTTGACAGAATTTGCCTACTGTGTGG
GGAACGGCTTGGAGGGGGTGTGGGCTTCAGGAGGCTGAGATGTCCTGTTTCTTGTGCCCC
CTCCTTTCTTCCCAACACCCGAGAAACCTGGATGGGTGTGGGGACCAGAGACCTGGAGGT
GGCCAGATTGGGCTTTGGCGGGACGCTTAGCAGCCCTCGGGACCTGTTCAGACTGCGGCC
TCCCACCTTCGGGAAGCATCGGCGCTGCCCATCTGCCCCTGCCTGGCGTCCAGGGAGTCC
CGGCTGTGCAGCGCTTCCCTTGAAATGTCTCTCTGTCCTCCCATCCAGTGCCTGGGACCC
GGCAGCGCCGTCGAGGCAGGGGGCTGCGAGGCGGGACCCAGTTGCACGTGGGCCCTGTGG
GGTCACTCCCTTTCGGGGGTCCTCTAGCTCTTCACCCTGCGCGCGTGGGGCAGACCAGAT
GCCTCGAGGAGCTCCAGGACCAGTGCCTATGGGGTAGTCCCTGCCGGCGGTGGGCCCCAG
TCCCAGACTGCGGCGCGCTATTTCTTTCTGGGGTTCGTGTGAGCGTGGGCTGCCAGAATG
GTGCCCACAAGCTGCTTTTGGGTGATTCAAATCATTTATACAGATAGTGCCCCTGCAAAA
AACATTTGCGCAGGGCCCCGCTTACGCCAGAGGATTGCGGGCCACTTCTGGGCATCGCTC
CTCGTGGGGATGGGAGCATCTCCCTGGAGAGCCCTTTGCAAAGGCCAAGCGCCGGCCAAA
GGCACACCGCTGGACGCGTTTCCTTCCTTCTGGAGAGATGACCAGGAATGCAGGATCCAA
AGGGGGTCTTGGAGGGAGGGCGGGAAGGGCATCTCCGGATCTGGGCAGACCCAGGGCTGC
CGGCTCCCCGAGGAGAATACGGGCTGGGGGCGAGGAGCCGGAGGGCAGGTCAGGCAGTGC
ATCAACCCTTGGCTCCTCCACCGCAGCCCCAGCCCGCAGGCTATCGCTCAGGCTTCTCTC
TCCGGGTTATGTAACCCCGGGACGGGACGTGGCAGCCGGGTGAGTGAGCGAAGGAGTAGG
GGAGGGAAGGGAAAGGAGAGGAGGGGCAGGGCCGGGCTTGGTGATGGTGGTGGTGGGAAG
CGCCGCCGTGCCGCCTCTTCTTGGGCCCCTTGGGTTGTCTTTCTGGAGGATTCCGGGACC
AGCCCTCTCCCCAGGCTCCGGGTCGCCCCCTAGCCCCCCGCCGCCTCATTTTCCCTTCAC
TCTTTTCCCCCTTCTGTCCCACCCGCCCTGCCAGGGGGCCTCTGGCTCTGGATAGCTTTT
CCTCTCCGGTTGTAGTTTCCTTCCCAAAGTTCTCAGCTTTGCTACCTCGCCCAAGTCATT
AGCCGCTCTGAGCCTCAGTTTATCAGTTTGTAAAATGAAGTTTGATTGAGCGGCCACGTG
TAAAACTCCTGGCATAGTGCATGGTACAAAGTAGATGTCTGCTGCAGGCTAAGGGCCTCG
AGGGGCTAAGTGAAATGTTGTGTGCCAGGCTGGGTGTCAGAGCCCCGGGAGCCGCAGCCA
CGAATGGTTGGCTCCCGGGTGGTAAAAGAATTTATCAACAACAGTATAGGTTTGAAAAGT
TTTATTAGATGGAAAGAACTCCACAGCAGAGCGCAGCGGGATGCTTCGGCAAGAGAGGCC

TGAGCTCACTTGCAGGGAACTGAAGGGTAATTTTGACCACATTAGTTTTGTAGGTCATAG
TAAATGATTACATTTGTAGACATTTTGGCACCTTGATGACAGCAAAGGTTGCACAATGGG
TTCCAACATGCGTGCATTCCGGAGATGTATAGAAATTCTAGGGAAAGAAGCCTGGTACCA
GATGTGGCTTTAGATAATAGGAAAGTACCATTCTGAGTTCTTCAGATAAGGTGCTTTGCC
TCCTGATGGTCTGCTTGATGGCCACCAGGTGATCCTTGCTCTCCTCATTTTCCCCCTGAT
AAATATTTTGGGCAAATCTTTGACCCTTTGTATTTCTCCATGCTCATGTCTACTTGTCTG
TTAGGATCCCAAGAAAGGGAAAATGGCACAGTGAAGAGGGGTGTCCAGTCTATCTGGCTA
CTTCCTGCTGAAAAGGGGCATTGAAAGGATTCCTTTCTTGCTTTCTGTCATGAAGGGAAT
GAAGGGTCATGATAAACTTGTTCATGGAGGGAAGACCAGATTCCATCAAGAGGCCCCATG
AAAATAGAAGTTGCTGTTGCAGGCTGGTATTGGGATTGCATAGTCATCTGTAGGTGGAAT
CATTGTAAGCTGGAAGATATAAGCATTAAAAGGCAGGAATTACCGGCATGCACCTCCATG
CCCACAGATTTTTGTGTTTTTAGTAGAGACAGGTTCTCACCATGTTGGCCAGGCTGGTCT
CCAACTCCTGACCTCAGGTGATCCGCCCGCCTCGCCTTGGTCTCCCAAAGTACTAGGATT
ACAGGTGTGAGCAACCACACCTGGCCCCTGGGGTCTCAATTTGTGTATTTATGCATGGCC
TCCACCAGTCTAGCTTGGAAAAGGGCAGGGCTTTCAGATAGTTTCATACATACAAAATTA
TTATTTCTTTTTATTTTATTTTATTTGAGATGGAATTTCGCTCTTGTTGCCCAGGCTGGA
GTGCAGTGGCGCAATCTCAGCTCACCACAACTTCCGCCTCCAAGGTTCAAACGATTCTCC
TGCCTCAGCCTCTGGAGTAACTGGGATTACAGGCATGCACCACCATGCCCAGCTCATTTT
GTATTTTTAGTAGAGATGGGGTTTCTCCGTGTTGGCTAGGCTGGTCTCAAACCTCAGGTG
ACCCGCTCGCCTCAGCCTCCCAAAGTGCTGGGATTACAGGTGTGAGCCACCGCGCCCAGC
TATTATTTCTTATAATTTAGAAAAATTAACAGGTTTTATTATATATTTTTCATTCCCTCC
AACAGAGAAGTTACCATATGATCCTGTCTGCCCTTACCTCTGTTTGGGCCAGAATTGGTG
GCCTGGTATTGCCAATAGGTTCTATGTTGGGGACAGCTTCTGCCCAGCTCTGTTATTAGG
ACTGGGAGCATGAGCTTCATCTGCCCATGCTGAAGATCACACGTGTGATTTTTTGTGTGT
GGGAACAGCAGGTAGTTAATACCACAAATACATCTTGCCAGGTTAAATCAAAGGCAACAG
TTAAAGTCTGAAATTCTTGAATGAACTTAGAGGGATCCTGACTAAATGAACCCAACTTGG
ATTGAATTTGCAAAAGATCAGACATGATCAGAAAAGGGACATGAACTTGGCTTGTTCCCA
AATCTTCATTAGCCACCTTAGGGAGAGGCAAAATATTTTGGGGATTTTTCTGAGGACTCT
GTACTAGTAGCATATGTGACTCCCCTGAGAGTATGTGAAGGGGAGAAAGTATTTGGGTAT
GTGGGTGGGAGATTGACTAGGGAATGGAGCAGATGGAGAGGGTGTAGGTGAAGAGTGAGC
AGGTTGAGGAGGATGTAATAGGCAAAAGGAAGGATCATCTAAGACATCAGAACCGGGAAG
GGAGGACGTTCCTTGGAAGCATACATGACAATTTGTATGTAATTTTGGGTTTGGATTTGG
GGATAAAGCAAAAAAGACCTGAACATATGGGACTTCTGAATCCTTTCCAAGGTTCCGGCA
AAAAATCAGTTAAGTTGTAAAGTAGCATTGCAATCCCAAGTTTCATTAATTGGCCAAATT
GATTGATTAGGGAGCTTGTATTGAACCCAAGCAATATTAGAAAAAAGGATATGCTTTTTA
AACTCTTATTTATTTTTTATTTGTATTTTTTGAGACAGAGTCTTGCTGTGTCGCCCAGGC
TGGAGTGCTGTGGCGCCATCTTGGCCCACTGCAACCTCCGCCCCCGGGGTACAAGTGATT
CTCCTGCCTCAGCCTCCCTAGTAGCTGGGATTATATGTGCCCGCCACATATAATTAGCCC
CCTGGCTGATTTTTTTTTTTTTTTTGTATTTTTAGTAGAGACAGGGTTTCGCCATGTTGG
CCAGGCTGATCTCGAACTCCTGACCTCAGGTGATCCACTCGCCTCGGCCTCCCAAAGTGC
TAGGATTACAGGTGTGAGTCACTGTGCCCGGCCAAGTTTTGCATTTTTAGTAGACTCCCG
GTCTTTAACTCCGGACCTCAGGTGATCTGCCTGCCTTGGCCTCCCAAAGTGCTGGGGTTA
CAGGCATAAGCCATTGTGCTCAGCCTTATATGCTTATTTTTAAGAGTTTGTGGGTCAAAA
TGAGACCAATGGGACCATTTTTAAGGAGGCAATCCAAGGGCGAGTTGGATGGAACTGAAT
TAATTGAACCGAAGTTGGGTTTAGACAAGGAACTACAAGATCCCTGAGGCATCCCTGTGT
AGAATTGAGATCCACCGCTTCCAGGACAAGGCTTATGGAGTGTTAAAATGAAAGTGCCCT
GCCACTCTGACAGGCAATAGCTCTTTTGTCTTGGCCTTGGGGTAATACCGGGGGATGGCG
CTTGGCCAGAAACTGTCAGTTGCCAACGAGAACTCAAGCTGGTTCACTGGCAGTCCGAAA
ACAGAAAAGAGCCCTGGCCAGTCCCTCACCCCTAAGGGCAAGGACAGCCAGGTATCCCTT
CTCTAGGGCTTCAGGATCCCACAGAAGAGCTGCCTCCACCGGGACCGGCAGTTCCCCAAA

GAGTAAAGAACCAGACCGTGGAAGGAAGCAGAGAGAAAAAGGAAGAGGGAAATCCCAGTG
AAGTCCCCGTATGGGCCACCAAGATGCCAGGCGAGGTGTCAGAGCTCCGGAACCGGGAAG
TGGTTGGCTCCCGGGTGGTAAAAGAACTTATCAACAACCGTGTAGGTCTGAAAAGGAAAG
TTTTATTAGACGGAAAGGACGAGGCAGCAGAGCGCAGTAGGCGCTTCAGCAAGAGAGGAC
TGAGCTCCCTGCGGGGAACTGCAGGGTAATTTGGACCACATTAGTCACTTAGGTCATGGT
AAATGGTTACATTTGTCGATATTTTGGTGCCTTGATGTCAGCAAAGTTTGCACAATGGGT
CTTAACGTGCACTCATTCCGGAAACGTACAGAAATTCTAGTTACTTATAAATTCTTGGGA
CGGAAGCTTGGTACCAGATGTGGCTTTAGACAATAGGGAAGTGTCATTCTGAATTGCTCA
GATAAGGGGCTTTGCCTCCTGTTGGTCGACTTGATGGCCACCAGGTGATCTCTGGTCTCT
TCAGTGTGGCTTTGCAGACTATAAAGGCGCAGCGCGCCAACGAGGCGGGTTGGCCCCAGA
CGGCGGAGAGGAAGGGCAGAGTCGGCGGTCCTGAGACTTGGGGCGGCCCCTTGGAGGTCA
GCCCCGCTCGCTCCTCCCGGCCCTCTCCTCCTCTCCGAGGTCCGAGGCGGGCAGCGGGCT
GTGGGCGGGCAGGAGGCTGCGGAGGGGCGGGGGGCAGGAAGGGGCGGGGGGCTCGGCGCA
CTCGGCAGGAAGAGACCGACCCGCCACCCGCCGTAGCCCGCGCGCCCCTGGCACTCAATC
CCCGCCATGTGGGGGCTCCTGCTCGCCCTGGCCGCCTTCGCGCCGGCCGTCGGCCCGGCT
CTGGGGGCGCCCAGGAACTCGGTGCTGGGCCTCGCGCAGCCCGGGACCACCAAGGTCCCA
GGCTCGACCCCGGCCCTGCATAGCAGCCCGGCACAGCCGCCGGCGGAGACAGCTAACGGT
GAGTTCCCCGACCGACGGTCCGCTCCCCCGCAAGCCGACTGCCCGGCTCTCCTGCCCCGT
GGGGCGATCCCTCCCTAACACGCGGGCACACGCACACCCACGCACACTCACAGTCATGCA
CACTCACCCCGCACGCACACTCGCACTCACGCGCACACACGCGCGCGCACTCACACACAT
TCACACACGCGCACACTTGCACTCACACGCGCGCGCATTCACACGCATGCACACACACGC
ACACTCACACGCGCGTGCGCGCACACACAGTGCACGCGCGCGCACACTCACACTCACAGT
GCACACACACATATACACACTCACACTCCCTCAACTCCCTGCTGGGAGCAATGGCTGCTG
ACTCGGCAGCCCCAGTTCCCTGCCAGACCTAGTCAGCAGTCCCAGGACAGGCGCCAGTGG
GATGCTGCCTCTTCCAAGCCCCAAACCTTCCCTTTTCACCAAAGACAAAACAGGCCAGAA
CTGGCAGGAGGGGAGACAGAGGGGCAGAAGCTCTCAAGGTGCAGAGCAAGACTGCGTAGG
AGAGAGTTTGAAGGCGAGGGCTGGAGAGAAAGAACAAAAGGAAAGAAGGGAGAGCCCCTC
GCTGAGGCTGCCGGGAGGATGGGGCAGAGCGGGAGAGGAAGGCAGCCCGACCTCCCAGCT
TTCCAGATGTGGAATAGGAGAGGAGGAGCGCAAGCGGAGGGCACTCAGGGGCTTCTAGAG
GAGGCAAGTGGAGGAGGGTCTTGAAGGGTGATGTCCCCGAGTCAGGGGAGTCTGGAGAGA
GAGAGAGAGAGAGGGCTGCCAAGAAGGAAGCGGCGGGCAAAGGCACAGGGGCACCAGATG
CGGAAATGGGCAGCCTGTTCTGGAGGCAGCTGTGGAGCTTCGATGGGTACCCCCAGCACC
TGCCTGGGCAGAGCCTTGTGCTGAAGGGCCGGCGGGCAGGCCCAGCCCTGAAAGCCTCGA
CACCCAGGCAGACATGGATTCCAGGACAGGCCATCTGAGCCCAGAGAGCAGACACAACAA
TGGAAGCGGCACAGGGGTTTTGGGGCATGATGCTGAGTCTGGAGCTAAGAAAGCCTCCTT
GGAAAGGCATCTGGGCTGAGATGCAAAGGAAGAATGGGAATTAGGTGAAAAAATCAGAGG
CGAGGGGTAGCATTACAGGGGAGGGGATAGCTAGTGCAGAGGCCCGGAGGTAAAGTGCCA
GACTCAGCTCTTTGGAGCAACCGAACAGTTTCTAGAGGCTGGGTGCAGCTCTCCATTGGA
TTAGAGGTTCACAGGGGAGGCTGGCCAAGCATGTAGTTACATCAGGGAGGAGAAGGAGGA
GCCAAGGAAGTGACTGGAGAGGCAGGTTGGGGTCAGATTGCAGGCCTTTGATGTCCTGTG
AAGGCTGTTAGATCCTGGTGGTGTGGCCTGCTGTGGGCTCACATGTCTTCTTGGGCTGGC
AGACCTTTCCATCCGGGGTTTCACCATTCTTCCTTTCCCCCATGCTGTGCCTCTCGGACC
CCAAGGGACCTCAGAACAGCATGTCCGGATTCGAGTCATCAAGAAGAAAAAGGTCATTAT
GAAGAAGCGGAAGAAGCTAACTCTAACTCGCCCCACCCCACTGGTGACTGCCGGGCCCCT
TGTGACCCCCACTCCAGCAGGGACCCTCGACCCCGCTGAGAAACAAGAAACAGGTACTTC
CTCTCCAGGGGCCCAGCCCAGACTTGCAGCCCCTGGGGCACTTTACCAGCACAGCTCTTG
GCCTCATGGGCACCGGCACGCCCCTTGCTTGCCTAGCGCAGGAGCAACCTTAGGCTCAGC
TTCCCACCTGCCCTGGCTACCCTCCCTCTGGTCCTGTCTCACTGTTCTATCCCCGCCCCA
GGCTGTCCTCCTTTGGGTCTGGAGTCCCTGCGAGTTTCAGATAGCCGGCTTGAGGCATCC
AGCAGCCAGTCCTTTGGTCTTGGACCACACCGAGGACGGCTCAACATTCAGGTCAGTAAT

CCTGGCTCGGAGCCATGGTCTCAGGGTAGGGAAGGCAGCCCCTGGGAGCTTCTCTCCTGC
CTCCTCTCTGTCCTGGCCTGCCCCACTCTGTCCAACTGGGCCTGACCACCATGTCCTGTG
TCTGCAGTCAGGCCTGGAGGACGGCGATCTATATGATGGAGCCTGGTGTGCTGAGGAGCA
GGACGCCGATCCATGGTTTCAGGTGGACGCTGGGCACCCCACCCGCTTCTCGGGTGTTAT
CACACAGGGCAGGAACTCTGTCTGGAGGTGAGGCAGACTAACCCTAGGTCAGGAGGTCAC
AGAAGGACTGGGGTGGGAGTCCTGGGGGCACCGATGATCTCTCTCCACCTCTCCTGCCAG
GTATGACTGGGTCACATCATACAAGGTCCAGTTCAGCAATGACAGTCGGACCTGGTGGGG
AAGTAGGAACCACAGCAGTGGGATGGACGCAGTGAGTGGTCCCACTGTGGCTGGGGCCTC
CATGCTGGGAGTTGGGCACCCAGTCCAGGCTAGGCTGAGGCTCCTCTGAGGACAAGGAAT
AGACGCCAGCTTAGGCTTCCCAGGGGGGTGTGGCTTGTTGTCAAGAGGGTGGCACACGGC
AGGCACCATTGGGAGCCAGCTGCTTTGGGACATGCCCACATCCTCCCCAGATAATGCCAC
CACAGGGTGGGTGCTGCTTCACGGTACAGCTTCCTCCTGGCGTGCCCCTTCTGGCCCGGG
GCCTCTGGTCCACATCACTTCTTGCCTTCTCGTGGTTCTGACTTCCGCATCTCATGGACC
TCTTTTTACAGCAGGCTACAATGTGGAGTCCTGGCCAGCTCTAGGATTGGCTTCCCCCGA
GTCATGTGGCCAAACTGGTCTAATGAACTGTGTCCAATCCAGAGAGCAAGGCTGCCTAGG
GCTGCCCATTGGCAGGGGCTGTGGGCCGGGGTCTGTGTTTGATGCACAGTGCAAGTCTCT
AGCTGAGCCCACTAGGGTGGGGAGACAGTAAGCTTGGAGGCCTGAGCTCCTTCCCTGGGT
CCTGGGCCAGGCTTCTGGGGTTTGAGCAGCCACAACAGAGAACTTGCTGCCCCCAGGTAT
TTCCTGCCAATTCAGACCCAGAAACTCCAGTGCTGAACCTCCTGCCGGAGCCCCAGGTGG
CCCGCTTCATTCGCCTGCTGCCCCAGACCTGGCTCCAGGGAGGCGCGCCTTGCCTCCGGG
CAGAGATCCTGGCCTGCCCAGTCTCAGGTGGGCAGTCAGGCCAGGGTTGGTTGGGCAGGG
CTTGGATGCAGGGTGCATCCTTCACTGTGGACACACCCTTTACCATAAACTCAACCTCCA
CCAGACCCCAATGACCTATTCCTTGAGGCCCCTGCGTCGGGATCCTCTGACCCTCTAGAC
TTTCAGCATCACAATTACAAGGCCATGAGGAAGGTCAGATATAACCCCTATGACCTGGGA
AGGAGGGCCCACCCATCTCAGGTCCCCTTCCCACCTTCCCACCGGGGCACAACCTGCTGT
GACTGCGCTTGTATGCCCCTGCTGCCTCCTGATGTCTCAGCCTTCTCTCCTGTGGACCCC
TAAGCTCCATCCCACTTTCCCTTATTATGGCGCCCCCCCAGTCCTACCCCTTCCTCCCGG
CTCTGCTGCCGCTCCCCTCCTGTACCATGATGGGATGCCCCCTCTGTGTGGGCCATCGCT
GACTTTTTAAGTCTTTCCATGGCACATGTGATCTGCCCCTGGGTGTACCCCTCCCATGCC
TCATGCCACGCTACACTCTGCCCACCAGCTGATGAAGCAGGTACAAGAGCAATGCCCCAA
CATCACCCGCATCTACAGCATTGGGAAGAGCTACCAGGGCCTGAAGCTGTATGTGATGGA
AATGTCGGACAAGCCTGGGGAGCATGAGCTGGGTACTGGCATGGGGAGTGGGGAGAGGTA
GGCACAGGGCAGGGCCCCAGGCATGAACCCGCTGCAAGCCCCCATGTGTCCCCAGGGGAG
CCTGAGGTGCGCTACGTGGCTGGCATGCATGGGAACGAGGCCCTGGGGCGGGAGTTGCTT
CTGCTCCTGATGCAGTTCCTGTGCCATGAGTTCCTGCGAGGGAACCCACGGGTGACCCGG
CTGCTCTCTGAGATGCGCATTCACCTGCTGCCCTCCATGAACCCTGATGGCTATGAGATC
GCCTACCACCGGGTAGGCCACCCAGCATGAGGGCCACTCTGTCCTTCTGCCCTGGTGGCT
GGACCTGCTCGACTTGAACAAGCCTCTTGCCCGGCAGGGTTCAGAGCTGGTGGGCTGGGC
CGAGGGCCGCTGGAACAACCAGAGCATCGATCTTAACCATAATTTTGCTGACCTCAACAC
ACCACTGTGGGAAGCACAGGACGATGGGAAGGTGCCCCACATCGTCCCCAACCATCACCT
GCCATTGCCCACTTACTACACCCTGCCCAATGCCACCGTGAGTATTTTGAGGGCGGCAGT
GGAGGTCTGTGGGGGGCGGACCTTGTCTCTGTCTCCTGCCCCTCCTGACCTGCCCCATCC
AGGTGGCTCCTGAAACGCGGGCAGTAATCAAGTGGATGAAGCGGATCCCCTTTGTGCTAA
GTGCCAACCTCCACGGGGGTGAGCTCGTGGTGTCCTACCCATTCGACATGACTCGCACCC
CGTGGGCTGCCCGCGAGCTCACGCCCACACCAGATGATGCTGTGTTTCGCTGGCTCAGCA
CTGTCTATGCTGGCAGTAATCTGGCCATGCAGGACACCAGCCGCCGACCCTGCCACAGCC
AGGACTTCTCCGTGCACGGCAACATCATCAACGGGGCTGACTGGCACACGGTCCCCGGGA
GTATGTGCCTGAGGGTGGAGTTAGCCCTGGCCCCGTAACCCCCGCCCTGATAAGACAGCC
TGCGGTTGCGTACAGTGCTGGCGTCTGTTCCCACTCTGAAGTGTCCCTCAGAGAAGGGAG
GGTAGCGGGAGGATGGGACCGCATCCCGCCTGCTTAGGCAGCAGTGTCTGTGGTCCCCTT

AGGCATGAATGACTTCAGCTACCTACACACCAACTGCTTTGAGGTCACTGTGGAGCTGTC
CTGTGACAAGTTCCCTCACGAGAATGAATTGCCCCAGGAGTGGGAGAACAACAAAGACGC
CCTCCTCACCTACCTGGAGCAGGTCGGATCTGCGTCCCGGCCCCCAGCCTGCCTGAATCA
CTCCTGCTGTCCATTTAGGCTACAGCTCCTACCAGGGGTTCTTCTAAGGTCCAGCTGAGC
ATTCAGACTCACAAGATGCCATGGGCCATGCTTGGTATCAGATTGTCTTGGAAGCACACA
GGACAGGAAGTGCAGTTTGCTGGCAGCGTGGCATCGTGTTAGAGCCGGTGGGAGGAGCCT
CCATTGCAGTCTAGGTGGTGGTCCGTGGCGCTGCCCCAGAGCTATCCTCAGGAGAGACTC
ACGTGAGGCAGGTGCAGGAGCTGTCCTGGCATAGAAGCTTCATGTTCCATGGAGCTCATA
ACCCTTGTAATAGCTCCATAAGCAGAGCTTCCAAAGGGTCTACCAAAGACAAGCCCAATA
ACCTGGGAAAGCCCAAGGATAGATAAGCCTTCCTACCAGGTATTTATCATTTTCTTAGTC
CAGATGTGATTTGTCAATCAGGATTTCTTTTTTTTTTTTCTTCCAGAAGTAGTGTCACCT
AGGAACACAGTAGACCTACCACTTTGCTCAGGTTTGCAGGGCAACAGAGCCAGCAAGTTA
GCTAAACAGCACATTATCCTGCCGAAGGGGAAGGGCTCTGATAACCTCTTCCCACACAGG
TGCGCATGGGCATTGCAGGAGTGGTGAGGGACAAGGACACGGAGCTTGGGATTGCTGACG
CTGTCATTGCCGTGGATGGGATTAACCATGACGTGACCACGGGTGTGTTTGACCGGGAGG
GCAAGGGAAGGGGCTGGAGGGCTGGAGGCTCGGGAAGAAGCAGAAGATCATTAATTGGGT
CCTGATCGTGCCCTTCACTCTCCTCAGCGTGGGGCGGGGATTATTGGCGTCTGCTGACCC
CAGGGGACTACATGGTGACTGCCAGTGCCGAGGGCTACCATTCAGTGACACGGAACTGTC
GGGTCACCTTTGAAGAGGGCCCCTTCCCCTGCAATTTCGTGCTCACCAAGACTCCCAAAC
AGAGGCTGCGCGAGCTGCTGGCAGCTGGGGCCAAGGTGCCCCCGGACCTTCGCAGGCGCC
TGGAGCGGCTAAGGGGACAGAAGGATTGATACCTGCGGTTTAAGAGCCCTAGGGCAGGCT
GGACCTGTCAAGACGGGAAGGGGAAGAGTAGAGAGGGAGGGACAAAGTGAGGAAAAGGTG
CTCATTAAAGCTACCGGGCACCTTAGCTCATCTTCGTGTTGTCTCTGTGCCCCAGGTCCT
CCCCCCGGGGGCGGGCCTCGGCCCAGCCCTCAGTTCCTATTCTGCACACTTGCACACTCT
CATCAGTTGGCTTCTGGACACATTGTGTGAAAAGAGGATCCCACCTGGGCTCTTCTTGAA
CCAAGGGCCTGGCAGAGCAACTCATTTCTTCTGATCAGCTTCTGCTACAGGTACCATTAC
ACTGCTGCCAGGCATTCTGTAAGCGCCTGCTCATTGCCAGGTGTGCAAGGAATCAGGATC
AGCCGTGCCTGCACTCAAACTCCTGGGGCTCCTAGTCAAGGGAAAGGACAGTTCGGTACA
TTGTGAGACATGCTAGGGTGGAGGCCAGGTGCCGTGAGAGTGCAGGGGAGCTGCACACGT
GAAATACAGCACTGCACATCAACAGGACTGGGGCAGTCAAGGATGCAATAGAAGTAGTGG
CTCTAGAAGTTCAGGCGGGAGGTGGGCAGGGTGTGGAGTATGGACAGGGATGGCTCCAAG
GAGGAGGGTCAGCCAAAGGTGGGTCAGCTGAGAACATTTGAATTTGCTTCAGCCATTCTC
AGAGTATTGATAACTGATAGGCTTTGCTGAGTTTCTATCAGACTGAAGGGGAAGTTGTGT
ATCAGTCTGTGTCTTGCCAGGTAAACAACCCATTCTAGGCACTTAAAGTGGAGGGAAATT
TAATGCTGGAAATTGGATAGGAAGGTGTTGGAAGAGCTGGATGAGGCCGGGTGTGGTGGC
TCACACCTGTAATCCCAGCACTTTGGGAGGCTGAGGTGGGAGGATTGCTTGAGCCCAGGA
GTTTGAGACCAGCCTGGATAACATAGCCAAACCCCGCCTCTACAAAAATAAGAAATAAGA
AACATAGCCAGCTGTAGTGGCGCATGGCTAAGGGAGGCAGAGGCAGGAGGATCACTGGAG
CCTGGGAGGTGGAGGCTGCAGAGGCAGCAGTGAGCCATGATGGCGCCACTATACTCCAAC
CTGGATGGTCATAACAAAATAAACAAAAAA (SEQ ID NO:3)

FIG 9

>CG54007-04

ATGTGGGGGCTCCTGCTCGCCCTGGCCGCCTTCGCGCCGGCCGTCGGCCCGGCTCTGGGG 60
GCGCCCAGGAACTCGGTGCTGGGCCTCGCGCAGCCCGGGACCACCAAGGTCCCAGGCTCG 120
ACCCCGGCCCTGCATAGCAGCCCGGCACAGCCGCCGGCGGAGACAGCTAACGGGACCTCA 180
GAACAGCATGTCCGGATTCGAGTCATCAAGAAGAAAAAGGTCATTATGAAGAAGCGGAAG 240
AAGCTAACTCTAACTCGCCCCACCCCACTGGTGACTGCCGGGCCCCTTGTGACCCCCACT 300
CCAGCAGGGACCCTCGACCCCGCTGAGAAACAAGAAACAGGCTGTCCTCCTTTGGGTCTG 360
GAGTCCCTGCGAGTTTCAGATAGCCGGCTTGAGGCATCCAGCAGCCAGTCCTTTGGTCTT 420
GGACCACACCGAGGACGGCTCAACATTCAGTCAGGCCTGGAGGACGGCGATCTATATGAT 480
GGAGCCTGGTGTGCTGAGGAGCAGGACGCCGATCCATGGTTTCAGGTGGACGCTGGGCAC 540
CCCACCCGCTTCTCGGGTGTTATCACACAGGGCAGGAACTCTGTCTGGAGGTATGACTGG 600
GTCACATCATACAAGGTCCAGTTCAGCAATGACAGTCGGACCTGGTGGGGAAGTAGGAAC 660
CACAGCAGTGGGATGGACGCAGTATTTCCTGCCAATTCAGACCCAGAAACTCCAGTGCTG 720
AACCTCCTGCCGGAGCCCCAGGTGGCCCGCTTCATTCGCCTGCTGCCCCAGACCTGGCTC 780
CAGGGAGGCGCGCCTTGCCTCCGGGCAGAGATCCTGGCCTGCCCAGTCTCAGACCCCAAT 840
GACCTATTCCTTGAGGCCCCTGCGTCGGGATCCTCTGACCCTCTAGACTTTCAGCATCAC 900
AATTACAAGGCCATGAGGAAGCTGATGAAGCAGGTACAAGAGCAATGCCCCAACATCACC 960
CGCATCTACAGCATTGGGAAGAGCTACCAGGGCCTGAAGCTGTATGTGATGGAAATGTCG 1020
GACAAGCCTGGGGAGCATGAGCTGGGGGAGCCTGAGGTGCGCTACGTGGCTGGCATGCAT 1080
GGGAACGAGGCCCTGGGGCGGGAGTTGCTTCTGCTCCTGATGCAGTTCCTGTGCCATGAG 1140
TTCCTGCGAGGGAACCCACGGGTGACCCGGCTGCTCTCTGAGATGCGCATTCACCTGCTG 1200
CCCTCCATGAACCCTGATGGCTATGAGATCGCCTACCACCGGGGTTCAGAGCTGGTGGGC 1260
TGGGCCGAGGGCCGCTGGAACAACCAGAGCATCGATCTTAACCATAATTTTGCTGACCTC 1320
AACACACCACTGTGGGAAGCACAGGACGATGGGAAGGTGCCCCACATCGTCCCCAACCAT 1380
CACCTGCCATTGCCCACTTACTACACCCTGCCCAATGCCACCGTGGCTCCTGAAACGCGG 1440
GCAGTAATCAAGTGGATGAAGCGGATCCCCTTTGTGCTAAGTGCCAACCTCCACGGGGGT 1500
GAGCTCGTGGTGTCCTACCCATTCGACATGGTGACTGCCAGTGCCGAGGGCTACCATTCA 1560
GTGACACGGAACTGTCGGGTCACCTTTGAAGAGGGCCCCTTCCCCTGCAATTTCGTGCTC 1620
ACCAAGACTCCCAAACAGAGGCTGCGCGAGCTGCTGGCAGCTGGGGCCAAGGTGCCCCCG 1680
GACCTTCGCAGGCGCCTGGAGCGGCTAAGGGGACAGAAGGAT**TGA** (SEQ ID NO:5) 1725

FIG. 10

>CG54007-04

MWGLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60
EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL 120
ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH 180
PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL 240
NLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH 300
NYKAMRKLMKQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGEHELGEPEVRYVAGMH 360
GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDGYEIAYHRGSELVG 420
WAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYYTLPNATVAPETR 480
AVIKWMKRIPFVLSANLHGGELVVSYPFDMVTASAEGYHSVTRNCRVTFEEGPFPCNFVL 540
TKTPKQRLRELLAAGAKVPPDLRRRLERLRGQKD (SEQ ID NO:6) 574

FIG. 11

>CG54007-05

ATGTGGGGGCTCCTGCTCGCCCTGGCCGCCTTCGCGCCGGCCGTCGGCCCGGCTCTGGGG 60
GCGCCCAGGAACTCGGTGCTGGGCCTCGCGCAGCCCGGGACCACCAAGGTCCCAGGCTCG 120
ACCCCGGCCCTGCATAGCAGCCCGGCACAGCCGCCGGCGGAGACAGCTAACGGGACCTCA 180
GAACAGCATGTCCGGATTCGAGTCATCAAGAAGAAAAAGGTCATTATGAAGAAGCGGAAG 240
AAGCTAACTCTAACTCGCCCCACCCCACTGGTGACTGCCGGGCCCCTTGTGACCCCCACT 300
CCAGCAGGGACCCTCGACCCCGCTGAGAAACAAGAAACAGGCTGTCCTCCTTTGGGTCTG 360
GAGTCCCTGCGAGTTTCAGATAGCCGGCTTGAGGCATCCAGCAGCCAGTCCTTTGGTCTT 420
GGACCACACCGAGGACGGCTCAACATTCAGTCAGGCCTGGAGGACGGCGATCTATATGAT 480
GGAGCCTGGTGTGCTGAGGAGCAGGACGCCGATCCATGGTTTCAGGTGGACGCTGGGCAC 540
CCCACCCGCTTCTCGGGTGTTATCACACAGGGCAGAGATCCTGGCCTGCCCAGTCTCAGA 600
CCCCAA**TGA**CCTATTCCTTGAGGCCCCTGCGTCGGGATCCTCTGACCCTCTAGACTTTCA 660
GCATCACAATTACAAGGCCATGAGGAAGCTGATGAAGCAGGTACAAGAGCAATGCCCCAA 720
CATCACCCGCATCTACAGCATTGGGAAGAGCTACCAGGGCCTGAAGCTGTATGTGATGGA 780
AATGTCGGACAAGCCTGGGGAGCATGAGCTGGGGGAGCCTGAGGTGCGCTACGTGGCTGG 840
CATGCATGGGAACGAGGCCCTGGGGCGGGAGTTGCTTCTGCTCCTGATGCAGTTCCTGTG 900
CCATGAGTTCCTGCGAGGGAACCCACGGGTGACCCGGCTGCTCTCTGAGATGCGCATTCA 960
CCTGCTGCCCTCCATGAACCCTGATGGCTATGAGATCGCCTACCACCGGGGTTCAGAGCT 1020
GGTGGGCTGGGCCGAGGGCCGCTGGAACAACCAGAGCATCGATCTTAACCATAATTTTGC 1080
TGACCTCAACACACCACTGTGGGAAGCACAGGACGATGGGAAGGTGCCCCACATCGTCCC 1140
CAACCATCACCTGCCATTGCCCACTTACTACACCCTGCCCAATGCCACCGTGGCTCCTGA 1200
AACGCGGGCAGTAATCAAGTGGATGAAGCGGATCCCCTTTGTGCTAAGTGCCAACCTCCA 1260
CGGGGGTGAGCTCGTGGTGTCCTACCCATTCGACATGACTCGCACCCCGTGGGCTGCCCG 1320
CGAGCTCACGCCCACACCAGATGATGCTGTGTTTCGCTGGCTCAGCACTGTCTATGCTGG 1380
CAGTAATCTGGCCATGCAGGACACCAGCCGCCGACCCTGCCACAGCCAGGACTTCTCCGT 1440
GCACGGCAACATCATCAACGGGGCTGACTGGCACACGGTCCCCGGGAGCATGAATGACTT 1500
CAGCTACCTACACACCAACTGCTTTGAGGTCACTGTGGAGCTGTCCTGTGACAAGTTCCC 1560
TCACGAGAATGAATTGCCCCAGGAGTGGGAGAACAACAAAGACGCCCTCCTCACCTACCT 1620
GGAGCAGGTGCGCATGGGCATTGCAGGAGTGGTGAGGGACAAGGACACGGAGCTTGGGAT 1680
TGCTGACGCTGTCATTGCCGTGGATGGGATTAACCATGACGTGACCACGGCGTGGGGCGG 1740
GGATTATTGGCGTCTGCTGACCCCAGGGGACTACATGGTGACTGCCAGTGCCGAGGGCTA 1800
CCATTCAGTGACACGGAACTGTCGGGTCACCTTTGAAGAGGGCCCCTTCCCCTGCAATTT 1860
CGTGCTCACCAAGACTCCCAAACAGAGGCTGCGCGAGCTGCTGGCAGCTGGGGCCAAGGT 1920
GCCCCCGGACCTTCGCAGGCGCCTGGAGCGGCTAAGGGGACAGAAGGATTGA (SEQ ID NO:7)1972

FIG. 12

>CG54007-05

MWGLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60
EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL 120
ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH 180
PTRFSGVITQGRDPGLPSLRPQ (SEQ ID NO:8)202

FIG. 13

>CG54007-06

ATGTGGGGGCTCCTGCTCGCCCTGGCCGCCTTCGCGCCGGCCGTCGGCCCGGCTCTGGGG 60
GCGCCCAGGAACTCGGTGCTGGGCCTCGCGCAGCCCGGGACCACCAAGGTCCCAGGCTCG 120
ACCCCGGCCCTGCATAGCAGCCCGGCACAGCCGCCGGCGGAGACAGCTAACGGGACCTCA 180
GAACAGCATGTCCGGATTCGTGTCATCAAGAAGAAAAAGGTCATTATGAAGAAGCGGAAG 240
AAGCTAACTCTAACTCGCCCCACCCCACTGGTGACTGCCGGGCCCCTTGTGACCCCCACT 300
CCAGCAGGGACCCTCGACCCCGCTGAGAAACAAGAAACAGGCTGTCCTCCTTTGGGTCTG 360
GAGTCCCTGCGAGTTTCAGATAGCCGGCTTGAGGCATCCAGCAGCCAGTCCTTTGGTCTT 420
GGACCACACCGAGGACGGCTCAACATTCAGTCAGGCCTGGAGGACGGCGATCTATATGAT 480
GGAGCCTGGTGTGCTGAGGAGCAGGACGCCGATCCATGGTTTCAGGTGGACGCTGGGCAC 540
CCCACCCGCTTCTCGGGTGTTATCACACAGGGCAGGAACTCTGTCTGGAGGTATGACTGG 600
GTCACATCATACAAGGTCCAGTTCAGCAATGACAGTCGGACCTGGTGGGGAAGTAGGAAC 660
CACAGCAGTGGGATGGACGCAGTATTTCCTGCCAATTCAGACCCAGAAACTCCAGTGCTG 720
AACCTCCTGCCGGAGCCCCAGGTGGCCCGCTTCATTCGCCTGCTGCCCCAGACCTGGCTC 780
CAGGGAGGCGCGCCTTGCCTCCGGGCAGAGATCCTGGCCTGCCCAGTCTCAGACCCCAAT 840
GACCTATTCCTTGAGGCCCCTGCGTCGGGATCCTCTGACCCTCTAGACTTTCAGCATCAC 900
AATTACAAGGCCATGAGGAAGCTGATGAAGCAGGTACAAGAGCAATGCCCCAACATCACC 960
CGCATCTACAGCATTGGGAAGAGCTACCAGGGCCTGAAGCTGTATGTGATGGAAATGTCG 1020
GACAAGCCTGGGGAGCATGAGCTGGGGGAGCCTGAGGTGCGCTACGTGGCTGGCATGCAT 1080
GGGAACGAGGCCCTGGGGCGGGAGTTGCTTCTGCTCCTGATGCAGTTCCTGTGCCATGAG 1140
TTCCTGCGAGGGAACCCACGGGTGACCCGGCTGCTCTCTGAGATGCGCATTCACCTGCTG 1200
CCCTCCATGAACCCTGATGGCTATGAGATCGCCTACCACCGGGGTTCAGAGCTGGTGGGC 1260
TGGGCCGAGGGCCGCTGGAACAACCAGAGCATCGATCTTAACCATAATTTTGCTGACCTC 1320
AACACACCACTGTGGGAAGCACAGGACGATGGGAAGGTGCCCCACATCGTCCCCAACCAT 1380
CACCTGCCATTGCCCACTTACTACACCCTGCCCAATGCCACCGTGGCTCCTGAAACGCGG 1440
GCAGTAATCAAGTGGATGAAGCGGATCCCCTTTGTGCTAAGTGCCAACCTCCACGGGGGT 1500
GAGCTCGTGGTGTCCTACCCATTCGACATGACTCGCACCCCGTGGGCTGCCCGCGAGCTC 1560
ACGCCCACACCAGATGATGCTGTGTTTCGCTGGCTCAGCACTGTCTATGCTGGCAGTAAT 1620
CTGGCCATGCAGGACACCAGCCGCCGACCCTGCCACAGCCAGGACTTCTCCGTGCACGGC 1680
AACATCATCAACGGGGCTGACTGGCACACGGTCCCCGGGAGCATGAATGACTTCAGCTAC 1740
CTACACACCAACTGCTTTGAGGTCACTGTGGAGCTGTCCTGTGACAAGTTCCCTCACGAG 1800
AATGAATTGCCCCAGGAGTGGGAGAACAACAAAGACGCCCTCCTCACCTACCTGGAGCAG 1860
GTGCGCATGGGCATTGCAGGAGTGGTGAGGGACAAGGACACGGAGCTTGGGATTGCTGAC 1920
GCTGTCATTGCCGTGGATGGGATTAACCATGACGTGACCACGGCGTGGGGCGGGGATTAT 1980
TGGCGTCTGCTGACCCCAGGGGACTACATGGTGACTGCCAGTGCCGAGGGCTACCATTCA 2040
GTGACACGGAACTGTCGGGTCACCTTTGAAGAGGGCCCCTTCCCCTGCAATTTCGTGCTC 2100
ACCAAGACTCCCAAACAGAGGCTGCGCGAGCTGCTGGCAGCTGGGGCCAAGGTGCCCCCG 2160
GACCTTCGCAGGCGCCTGGAGCGGCTAAGGGGACAGAAGGAT**TGA** (SEQ ID NO:4) 2205

Figure 14.

```
>ptnr:SPTREMBL-ACC:Q9NUB5 DJ860F19.3 (NOVEL PROTEIN (ORTHOLOG OF MOUSE
           METALLOCARBOXYPEPTIDASE CPX-1)) - Homo sapiens (Human), 734 aa.
           Length = 734

 Score = 2735 (962.8 bits), Expect = 0.0, Sum P(2) = 0.0
 Identities = 510/510 (100%), Positives = 510/510 (100%)

Query:      1 MWGLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60
              MWGLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS
Sbjct:      1 MWGLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60

Query:     61 EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL 120
              EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL
Sbjct:     61 EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL 120

Query:    121 ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH 180
              ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH
Sbjct:    121 ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH 180

Query:    181 PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL 240
              PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL
Sbjct:    181 PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL 240

Query:    241 NLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH 300
              NLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH
Sbjct:    241 NLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH 300

Query:    301 NYKAMRKLMKQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGEHELGEPEVRYVAGMH 360
              NYKAMRKLMKQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGEHELGEPEVRYVAGMH
Sbjct:    301 NYKAMRKLMKQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGEHELGEPEVRYVAGMH 360

Query:    361 GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDGYEIAYHRGSELVG 420
              GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDGYEIAYHRGSELVG
Sbjct:    361 GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDGYEIAYHRGSELVG 420

Query:    421 WAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYYTLPNATVAPETR 480
              WAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYYTLPNATVAPETR
Sbjct:    421 WAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYYTLPNATVAPETR 480

Query:    481 AVIKWMKRIPFVLSANLHGGELVVSYPFDM 510  (Seq ID NO:45)
              AVIKWMKRIPFVLSANLHGGELVVSYPFDM
Sbjct:    481 AVIKWMKRIPFVLSANLHGGELVVSYPFDM 510

 Score = 341 (120.0 bits), Expect = 0.0, Sum P(2) = 0.0
 Identities = 67/69 (97%), Positives = 67/69 (97%)

Query:    507 PFD-MVTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPPDLRRR 565
              P D MVTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPPDLRRR
Sbjct:    666 PGDYMVTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPPDLRRR 725

Query:    566 LERLRGQKD 574 (SEQ ID NO:46)
              LERLRGQKD     (SEQ ID NO:41)
Sbjct:    726 LERLRGQKD 734 (SEQ ID NO:42)
```

Figure 15

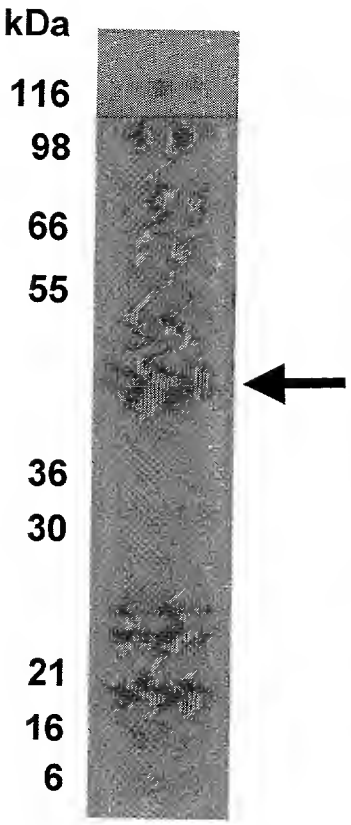
```
>ptnr:SPTREMBL-ACC:Q9NUB5 DJ860F19.3 (NOVEL PROTEIN (ORTHOLOG OF MOUSE
           METALLOCARBOXYPEPTIDASE CPX-1)) - Homo sapiens (Human), 734 aa.
           Length = 734

 Score = 1005 (353.8 bits), Expect = 4.4e-101, P = 4.4e-101
 Identities = 192/193 (99%), Positives = 193/193 (100%)

Query:     1 MWGLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60
             MWGLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS
Sbjct:     1 MWGLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60

Query:    61 EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL 120
             EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL
Sbjct:    61 EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL 120

Query:   121 ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH 180
             ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH
Sbjct:   121 ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH 180

Query:   181 PTRFSGVITQGRD 193 (SEQ ID NO:47)
             PTRFSGVITQGR+  (SEQ ID NO:43)
Sbjct:   181 PTRFSGVITQGRN 193 (SEQ ID NO:44)
```

Figure 16

```
>ptnr:SPTREMBL-ACC:Q9NUB5 DJ860F19.3 (NOVEL PROTEIN (ORTHOLOG OF MOUSE
           METALLOCARBOXYPEPTIDASE CPX-1)) - Homo sapiens (Human), 734 aa.
           Length = 734

 Score = 3952 (1391.2 bits), Expect = 0.0, P = 0.0
 Identities = 734/734 (100%), Positives = 734/734 (100%)

Query:     1 MWGLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60
             MWGLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS
Sbjct:     1 MWGLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60

Query:    61 EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL 120
             EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL
Sbjct:    61 EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL 120

Query:   121 ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH 180
             ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH
Sbjct:   121 ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH 180

Query:   181 PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL 240
             PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL
Sbjct:   181 PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL 240

Query:   241 NLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH 300
             NLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH
Sbjct:   241 NLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH 300

Query:   301 NYKAMRKLMKQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGEHELGEPEVRYVAGMH 360
             NYKAMRKLMKQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGEHELGEPEVRYVAGMH
Sbjct:   301 NYKAMRKLMKQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGEHELGEPEVRYVAGMH 360

Query:   361 GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDGYEIAYHRGSELVG 420
             GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDGYEIAYHRGSELVG
Sbjct:   361 GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDGYEIAYHRGSELVG 420

Query:   421 WAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYYTLPNATVAPETR 480
             WAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYYTLPNATVAPETR
Sbjct:   421 WAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYYTLPNATVAPETR 480

Query:   481 AVIKWMKRIPFVLSANLHGGELVVSYPFDMTRTPWAARELTPTPDDAVFRWLSTVYAGSN 540
             AVIKWMKRIPFVLSANLHGGELVVSYPFDMTRTPWAARELTPTPDDAVFRWLSTVYAGSN
Sbjct:   481 AVIKWMKRIPFVLSANLHGGELVVSYPFDMTRTPWAARELTPTPDDAVFRWLSTVYAGSN 540

Query:   541 LAMQDTSRRPCHSQDFSVHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE 600
             LAMQDTSRRPCHSQDFSVHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE
Sbjct:   541 LAMQDTSRRPCHSQDFSVHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE 600

Query:   601 NELPQEWENNKDALLTYLEQVRMGIAGVVRDKDTELGIADAVIAVDGINHDVTTAWGGDY 660
             NELPQEWENNKDALLTYLEQVRMGIAGVVRDKDTELGIADAVIAVDGINHDVTTAWGGDY
Sbjct:   601 NELPQEWENNKDALLTYLEQVRMGIAGVVRDKDTELGIADAVIAVDGINHDVTTAWGGDY 660

Query:   661 WRLLTPGDYMVTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPP 720
             WRLLTPGDYMVTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPP
Sbjct:   661 WRLLTPGDYMVTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPP 720

Query:   721 DLRRRLERLRGQKD 734 (SEQ ID NO:2)
             DLRRRLERLRGQKD
Sbjct:   721 DLRRRLERLRGQKD 734
```

Fig. 17

A.



B.

KKLTLTRPTPLVTAGPL

KKLTLTRPPPLV-AGPL

Figure 18 ClustalW alignment of CG54007-01, CG54007-04 and CG54007-05 proteins of the present invention.

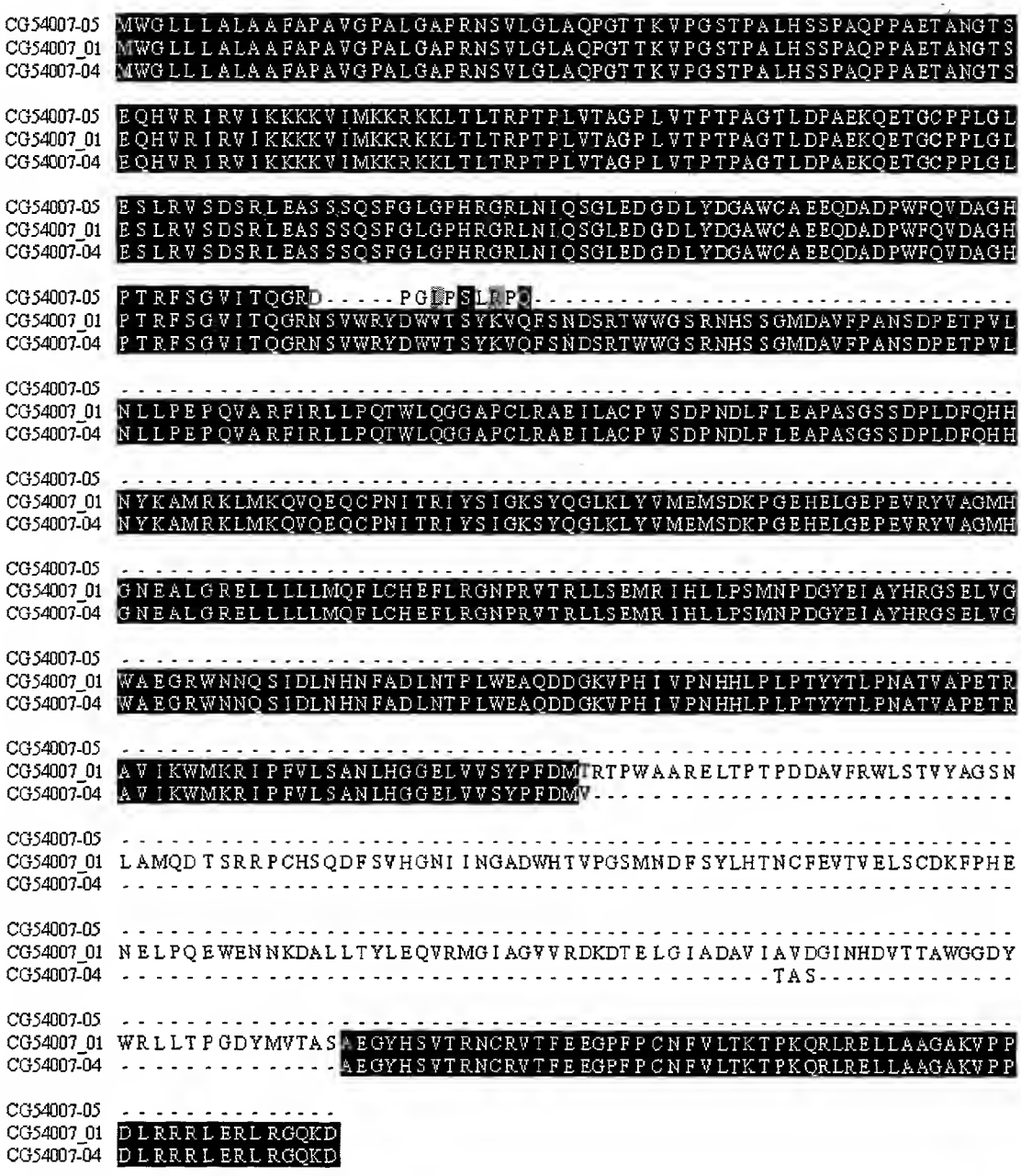


Fig.19

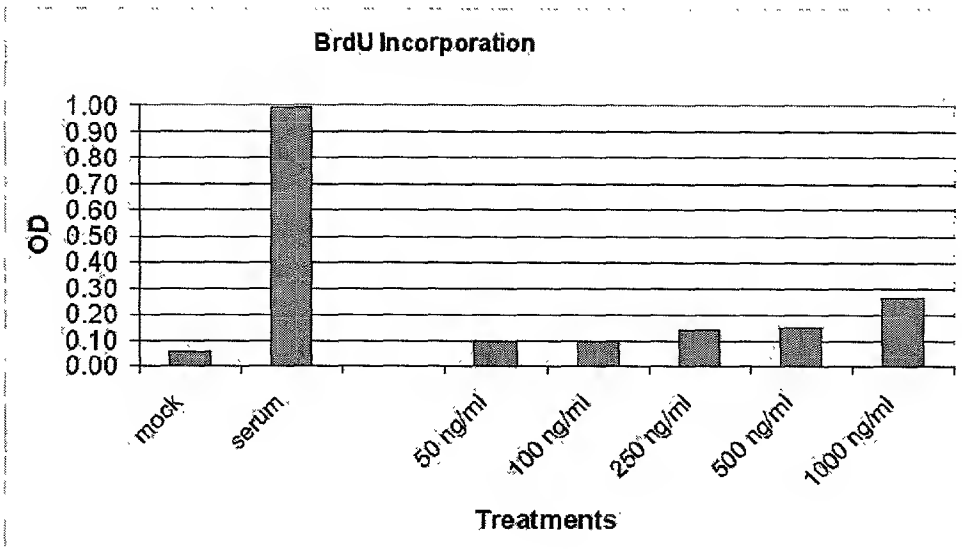
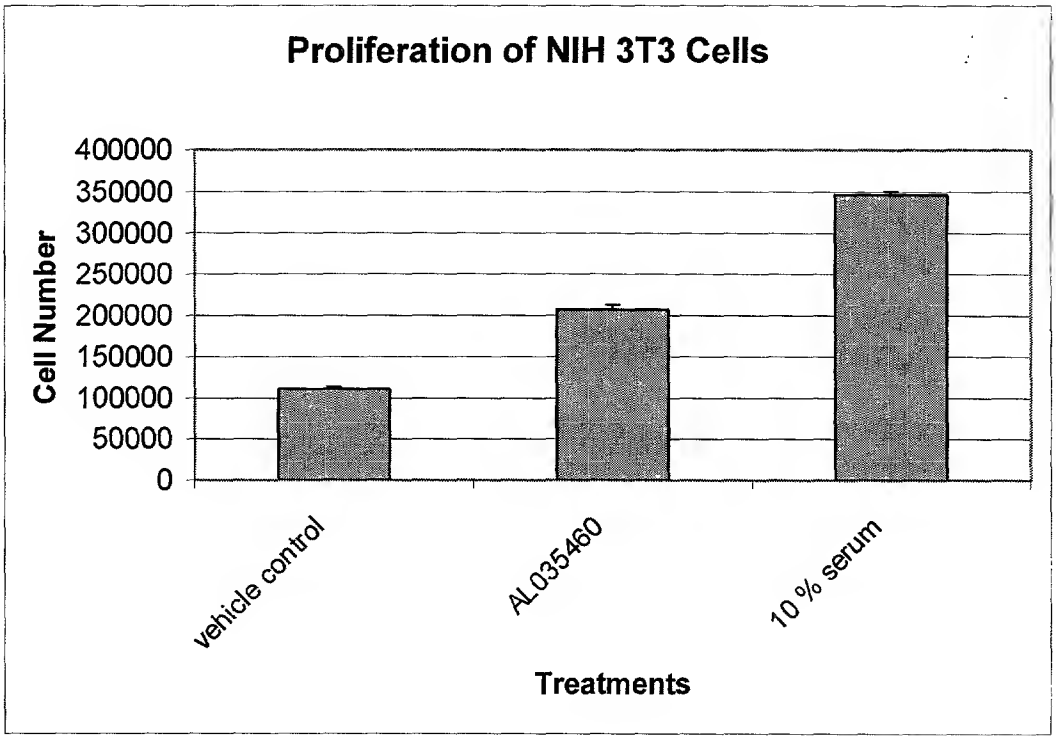

BrdU Incorporation
OD
1.00
0.90
0.80
0.70
0.60
0.50
0.40
0.30
0.20
0.10
0.00
mock
serum
50 ng/ml
100 ng/ml
250 ng/ml
500 ng/ml
1000 ng/ml
Treatments

Fig. 20


Proliferation of NIH 3T3 Cells
Cell Number
400000
350000
300000
250000
200000
150000
100000
50000
0
vehicle control
AL035460
10 % serum
Treatments